Plant Biotechnology for Health

From Secondary Metabolites to Molecular Farming



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María Alejandra Alvarez School of Pharmacy and Biochemistry CONICET/Universidad Maimónides Buenos Aires, Argentina

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Preface

In vitro plant cell cultures have provided a tool for studying plant metabolism and physiology and to explore productive processes of secondary metabolites.

More recently, genetic engineering has allowed the use of *in vitro* cultures to modulate plant biosynthetic pathways and to express heterologous proteins of biomedical relevance.

The aim of this book is to provide some background information about the potential of *in vitro* cultures for conducting phytofermentations and for molecular farming.

Also, the application of *in vitro* cultures for the production of the steroidal glycoalkaloid solasodine by *Solanum eleagnifolium* Cav. and the catalytic antibody 14D9 is reviewed. The expression of a recombinant glycoprotein E2 from BVDV in *N. tabacum* is reported.

I hope this book drive attention to the potentiality of *in vitro* plant cultures as a supply of compounds to be used for diagnostics and therapeutics.

I would like to thank Dr. Patricia Marconi and Dr. S. Klykov for their collaboration in the chapter related to mathematical modeling in recombinant plant systems. Also, I would like to thank the School of Pharmacy and Biochemistry of Universidad Maimónides and the National Agency of Promotion of Science and Technology (ANPCYT), from Argentina for their support.

Buenos Aires, Argentina 2014

María Alejandra Alvarez

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About the Author

María Alejandra Alvarez completed her studies at Universidad de Buenos Aires, Argentina. She graduated in Biochemistry in 1981 and Pharmacy in 1994 and obtained an MSc in Industrial Microbiology and Biotechnology in 1986 and a PhD in Plant Biotechnology in 1993.

She was lecturer in graduate and postgraduate courses of Botany, Pharmacobotany, Biotechnology, Food Biotechnology, and Galenic Pharmacy at Universidad de Buenos Aires, Universidad Nacional de La Plata, and Universidad Maimónides.

Dr. Alvarez started working on the production of compounds of pharmaceutical interest in *in vitro* plant cultures in 1986, being the author of numerous scientific articles. Her research interests include chemotaxonomy, medicinal plants, production of secondary metabolites, and molecular farming.

She was a researcher at Universidad de Buenos Aires and Centro de Ciencia y Tecnología Dr. César Milstein (CONICET/Fundación Pablo Cassará). Currently, she is a member of the National Council of Research and Technology (CONICET) in Argentina, Professor of Pharmacobotany and Pharmacognoscy and Director of the Plant Biotechnology Group at Universidad Maimónides, and Professor of Biology at Colegio Divino Corazón.

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Chapter 1 Plants for Health: From Secondary Metabolites to Molecular Farming

There is a continuous search of new drugs and molecules for health care. Plants offer a huge variety of those bioactive molecules, some of which are still unknown. Popular medicine is the source of information for ethnobotanists and pharmacobotanists, which in general are the first link in the chain that leads to the taxonomical, chemical and pharmacological description of a species.

Chapter 2 summarizes the classical strategy employed to analyze the occurrence of bioactive principles in plants, since their collection in the field to the analytical and biological assays. It also refers to the contribution of new technologies (e.g.: systems biology, synthetic biology) to the knowledge about medicinal plants, their active principles, and their specific contribution in the treatment of some pathologies.

Chapter 3 exposes the classification and main characteristics of plant secondary metabolites, giving some examples of their applications for health. The pharmaceutical industry profits from those bioactive molecules to elaborate or, taking plant compounds as starting point or model, to synthesize drugs with known or novel pharmacological activities.

The traditional sources of raw material are plants in the field. However, in the second half of the twentieth century the *in vitro* culture technology arise bringing the possibility of maintaining plant cultures in controlled environmental conditions, free from the risks of pathogen and predator attack, from weather variations, and from geopolitical circumstances. Chapter 4 describes the main characteristics and prospectives of *in vitro* cultures.

Chapter 5 reports the strategy employed to analyze the production of a solasodine, a steroidal glycoalkaloid, as an example of the approaches used to develop a productive process of a secondary metabolite in *in vitro* cultures.

By the end of the twentieth century the production of recombinant proteins in plants, named molecular farming, appeared as a new strategy for obtaining biopharmaceuticals. Numerous proteins were expressed (antibodies, antigens, blood proteins, growth factors, etc.) but, in most of the cases, the attained yields were not competitive to the traditional production platforms. There still more work to do before establishing a competitive production platform of plant-made biopharmaceuticals.

1

However, several companies are developing this technology and some products are in the pipeline or already in the market. Chapter 6 describes the basics of molecular farming and some of their applications.

Chapter 7 is about the expression of a whole recombinant antibody in plants, the catalytic antibody 14D9, which was taken as an experimental model to produce a recombinant protein in *in vitro* cultures. The expression of 14D9 was accomplished in undifferentiated *in vitro* cultures (calli and suspended cells), in hairy root cultures and a preliminary scale up to a 2-l bioreactor was performed.

Chapter 8 refers to the potential application of a recombinant immunogen, the truncated glycoprotein E2, transiently expressed in plants, to trigger a specific immune response and eventually to be used to formulate an experimental vaccine.

Finally, Chap. 9 gives a general view of mathematical modeling for producing recombinant proteins in *in vitro* cultures under Good Manufacturing Practices.

Chapter 2 Plants for Health

Abstract Humankind has been always employing plants as supply of food, textile, cosmetics, medicines, etc. Their chemical compounds have biological activities that are effective for the treatment of different human and animal diseases. So far, on an estimated number of 250,000–300,000 plant species only approximately 5,000 have been intensively studied for their medical properties. Ethnobotany and Bioprospecting can contribute to identify new plant species with potential pharmacological properties. When a new species is identified as potentially useful for health, two main approaches are practicable, one aiming to the search of an already existing biological activity that is in the market, the other to the random screening of any biological activity. Pharmacobotany, Pharmacognoscy and Phytochemistry, through a classical approach, contribute to identify chemicals and pharmacological activities by screening plant species using different fractioning methodologies, chemical assays and bioassays (in vitro, in vivo, ex vivo). New strategies as in silico predictions, which gather information about drug-target interactions and human diseases, System Pharmacology and Polypharmacology can increase the current knowledge on medicinal plants through novel approaches. A multidisciplinary work that integrates classical with new strategies will gradually have more impact in the identification of plant bioactive principles and their potential uses in health care.

Keywords Medicinal plants • Screening of plant active principles

2.1 Introduction

Plants are being used as source of food (cereals, legumes, vegetables, fruits, etc.), animal feeding (clover, millet, alfalfa, etc.), and essences for the elaboration of perfumes and flavors (rosemary, sage, lavender, mint, etc.). Also, plant resins and gums are employed in tanneries, woody species for construction and carpentry (oak, cedar, ebony, pine) and for the production of cellulose and paper (poplar, pine, fir). Other plant species produce textile fibers (linen, cotton and hemp) or are appreciated as ornamentals, e.g.: roses, orchids, tulips, dahlias, etc. (Table 2.1). Plants have also been used for obtaining medicines (e.g.: digital, aconite, rhubarb, belladonna, henbane, etc.), and people have been transferring the knowledge about plant properties and their employment from one generation to the next one (Teiten et al. 2013;

4 2 Plants for Health

Industry	Species	Use	
Food	Coffea arabiga	Beverage	
	C. sinensis var. sinensis C. sinensis var. Assamica	Flavor	
	Vanilla planifolia		
	V. tahitiensis		
	Piper spp. (Piperaceae)		
Cosmetic	Lythospermum erithroryzum	Dye	
	Lavandula spp.	Perfume	
	Mentha spp.	Flavor	
Pharmaceutical	Atropa belladona	Cardiotonic	
	Digitalis lanata		
Textile	Gossipium hirsutum	Fabric	
	Linus usitattissimum		
Agrochemical	Chrysanthemum cinenariaefolium	Insecticide	
	Calceolaria andina		
Construction and Carpentry	Schinopsis balansae	Wood	
	S. lorentzii		
	Quercus rober		
	Cedrus spp.		
	Pinus spp		

Table 2.1 Commercial uses of some plant species

Verpoorte et al. 2006). In the last centuries, the pharmaceutical industry has profited from the uncountable varieties of plant bioactive molecules to produce medicines and has synthesized molecules of similar biological activities. Aspirin was the first synthetic drug (1897), and was the starting point for the development of methods and technologies for synthesizing plant active principles or related compounds (Schmidt et al. 2008).

In Western countries, where chemistry is the backbone of the pharmaceutical industry, 25 % of the molecules used are of natural plant origin (Payne et al. 1991). On the other hand, the World Health Organization has estimated that more than 80 % of the world's population in developing countries depends primarily on herbal medicine for basic healthcare needs (Vines 2004).

2.2 Active Compounds from Plants

After a species is recognized as potentially useful for the pharmaceutical industry, their active principles and properties are studied. In some circumstances the crude plant extract or the pure active principle is directly employed as medicine. If the active chemical principles cannot be isolated or there is a shortage on raw material, the pharmaceutical industry focuses their efforts on producing that molecule by synthesis or semi-synthesis (Raskin et al. 2002; Balunas and Kinghorn 2005; Doughari 2012; Moronkola 2012).

2.3 Ethnobotany 5

Active principle	Source	Use
Artemisinina	Artemisia anua	Anti-malarial
Atropine, Hyosciamine,	Atropa belladonna	Anti-cholinergic
Scopolamine	Datura spp.	
Capsaicine	Capsicum spp.	Analgesic
Codeine, morphine	Papaver somniferum	Analgesic, Anti-tussive
Cocaine	Erytrhoxylum coca	Local analgesic
Cyanogenic glycosides	Manihot esculenta	
Digoxin, digitoxin	Digitalis spp.	Cardiotonic
Diosgenin	Dioscorea spp.	Steroidal contraceptive
Genistein	Glycina max	Anticancer
Nicotine	Nicotiana spp.	Anticancer
Pilocarpine	Pilocarpus jaborandi L.	Cholinergic
Psolaren, Xhanothotoxin	Apium graveolens	Anticoagulant
Quinine	Cinchona spp.	Anti-malarial
Reserpine	Rauwolfia serpentine L.	Anti-hypertensive, psychotropic
Taxol	Taxum brevifolia	Anti-neoplasic
Vinblastine, Vincristine	Catharantus roseus L.	Anti-neoplasic

Table 2.2 Active pharmaceutical compounds from plants

At the end of the twentieth century, from the new 3,500 novel chemical structures identified, 2,619 were isolated from superior plants. In the United States of America, 25 % of the market is based on plant-based compounds. What is more, most of the prescribed drugs of plant origin were initially used in popular medicine. Table 2.2 summarizes some plant-derived compounds of pharmaceutical interest.

Up to now, only 5,000 of plant species over an estimated number of 250,000–300,000 were intensively studied for their medical properties. Unfortunately, a great amount of them are in risk of extinction (Payne et al. 1991).

Ethonobotany and Bioprospecting have the potential to contribute to the discovery and conservation of plant sources of bioactive molecules.

2.3 Ethnobotany

The term Ethnobotany was coined in 1895 as "the study of plants used by primitive and aboriginal people" by the botanist Harsherberg. The term was extended years before to "the study of the interrelationships of primitive men and plants" (Jones 1941). Currently, it is defined as "the study of the relationships established between people and plants" (Albuquerque 1997) without specifying a particular time frame. What is for sure is that the information about the properties of plant species of a particular region gathered by ethnobotanists may be valuable to modern medicine. Those species can thus be used directly as a source of a medicine, as raw material for the semi-synthesis of bioactive compounds, as a model for the synthesis of new

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molecules, or as taxonomic markers for the discovery of new compounds (Gurib-Fakim 2006). In ancient times, naturalists, travelers, and missionaries collected information about habits and practices of people in distant and new discovered communities or tribes, which was often deposited in missions, monasteries, abbeys, etc. Ethnobotanists look in those documents and in archeological sites for information about the connections between ancient civilizations and towns with their plants. Those data reveal the migration habits, commercial routes, agricultural practices, and the origin and dispersion of those plant species. Ethnobotanists also study the relationship between people and plant species of today compiling the knowledge guarded by indigenous and rural people.

In Argentina, ethnobotany dates from the eighteenth century, when the Jesuits in the Missions collected information from the natives. The Plantae Diaphoricae Florae Argentinae (Hieronymus 1882) is considered as the first compilation of Argentinean plants in use. Domingo Parodi, Eduardo Matoso, Nicolás Rojas Acosta, Juan A. Domínguez, Lorenzo R. Parodi, Arturo Ragonese, and N. Martínez Crovetto made significant contributions to the matter (Pirondo and Keller 2012). Currently, numerous ethnobotanical studies were performed in different regions and communities of Argentina (Zardini 1984; Arenas 1997, 2012; Molares et al. 2009; Rosso 2013; Scarpa and Montani 2011; Suárez 2009).

2.4 Bioprospecting

Bioprospecting, or biodiversity prospecting, is the exploration of biological materials for commercially valuable genetic and biochemical properties. Local communities provide the information about collection and properties of those potentially valuable resources for the pharmaceutical, biotechnological, and agri-business fields. Bioprospecting supporters consider it as a means of preserving biodiversity, by financing its conservation, and of discovering new drugs for human health (Harvey and Gericke 2011). For supporting the sustainable use of biodiversity the United Nations Convention on Biological Diversity was created in Rio de Janeiro (1992) with the objective of preserving biodiversity, promoting the sustainable use of the components of biodiversity, and encouraging the sharing of benefits derived from the commercial and other uses of genetic biological resources in a fair and equitable way. In the USA, the NIH funded the International Cooperative Biodiversity Groups (ICBG) that coordinates cooperation programs involving the USA and countries with high biodiversity as Costa Rica, Indonesia, Panama, Papua New Guinea, Madagascar, the Philippines, and Vietnam. With the same goal, the Rutgers University funded the Global Institute for BioExploration, GIBEX. The Bonn Guidelines and the Nagoya Protocol also considered the non-monetary benefits related to the commercialization of natural resources (Castree 2003).

Usually, companies establish a financial agreement with countries with high biodiversity (e.g.: Costa Rica, Brazil), which is a point that leads to controversies about the inappropriate commercialization and to the approach used to valuate biodiversity 2.5 Screening 7

(Harvey and Gericke 2011). Detractors consider bioprospecting as "free market environmentalism" or as a "post modern ecological capitalism" highlighting the unfair distribution of benefits with local rural communities and the dubious preservation of biodiversity (Castree 2003).

On the other hand, bioprospecting supporters remark that, in the specific matter of health, bioprospecting can make available new plant species with active principles yet unknown.

2.5 Screening

When a new species is identified as potentially useful for health, two main approaches are practicable, one aiming to the search of a particular biological activity that already exist in the market, the other for the random screening of any biological activity. The first approach tests samples by standard methods; the second demands the realization of a set of bioassays.

The process (Fig. 2.1) starts as soon as the plant species is collected. First, the species has to be identified by a taxonomist, who has to deposit a sample in a botanical repository or herbarium. Immediately after, the plant material is dried, at room temperature or in an oven, preferably avoiding light exposure. Then, it is ground to very small particles or to powder to carry out the extraction of the active principles.

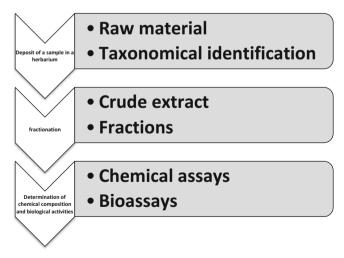


Fig. 2.1 General scheme for the extraction, isolation and characterization of active compounds from plants

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2.5.1 Extractive Process

When there is no clue about the chemical composition of the species, a preliminary extraction in different solvent systems is performed. An initial step of fractionation is followed by the identification in each fraction of its chemical compounds and activity.

2.5.1.1 Solvent Fractionation

Solvent fractionation is the process of separating the chemical compounds of a crude extract according to their different solubility, basically hydrophobicity/ hydrophilicity. In general, extraction is tested in a sequence of solvents of increasing polarity (Katiyar et al. 2012) (Fig. 2.2). The extraction can be performed at room temperature, at high temperatures under reflux, using supercritical fluid or Soxhlet. The extract is then concentrated several times and stored for further studies, in general at low temperatures ($-20~^{\circ}$ C) to minimize degradation.

2.5.1.2 Chromatographic Fractionation

The chromatographic techniques most used are Thin Layer Chromatography (TLC), High Performance Liquid Chromatography (HPLC), Gas Chromatography (GC),

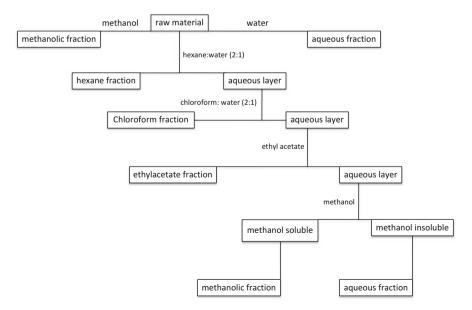


Fig. 2.2 Example of a solvent fractionation scheme

2.5 Screening 9

Size Exclusion Chromatography (SEC), etc. In occasions a combination of different techniques and methods are utilized, as HPLC coupled to electron impact-mass spectrometry (Weber et al. 2007).

2.5.1.3 Bioactivity Guided Fractionation

The use of bioassays as fractionation monitors has been the most common strategy to identify bioactive molecules. Limitations to this approach are the presence of interferences, loss of activity during the process of fractionation, and low solubility and instability of the principle of interest (Houghton et al. 2007).

2.5.2 Chemical Screening

Chemical species are identified by standard techniques (Table 2.3). The results provide preliminary information that give information and orientation for the subsequent bioassays. The screening can be performed in the crude plant extracts or in the fractions resulting from the partition through different methods (Tiwari et al. 2011).

2.5.3 Bioassays

The identification of the compounds with biological activity must be performed using sensitive bioassays, which must be simple, reproducible, fast and the least expensive possible. Those assays are performed on the crude extract or in the fractionated extract. Sometimes bioassays are not predictive for clinical efficiency, which makes extremely helpful to perform complementary analysis (Hostettmann 1999).

Chemical group	Standard test	
Alkaloids	Mayer's, Wagner's, Draggendorff's, Hager's	
Carbohydrates	Molisch's, Benedict's, Fehling's	
Glycosides	Modified Borntrager's	
Saponins	Froth's, Foam test	
Phytosterols	Salkowski's, Liberman Buchard's	
Phenols	Ferric chloride test	
Tannins	Gelatine test	
Flavonoids	Alkaline reagent test, Lead acetate test	
Proteins and aminoacids	Xanthoproteic test, Ninhydrin test, Bradford's	
Diterpenes	Copper acetate test	

Table 2.3 Some usual techniques for detecting chemical groups

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Activity	Method
Radical scavengers and antioxidant	Ferric reducing ability of plasma assay (FRAP). Benzie and Strain (1996) Spraying of TLC plates with 2,2-diphenyl-1- picryl hydrazyl (DPPH) radical
Antibacterial	Measurement of inhibition zones on microbial lawns grown in nutrient agar
Antifungal	Microbroth dilution assay following the Guidelines of the National Committee for Clinical and Laboratory Standards (NCCLS) for yeasts M-27-A2 (NCCLS 2002a) and filamentous fungi M-38-A (NCCLS 2002b)
Toxicity	Assay with the crustacean <i>Artemia salina</i> Leach. Mortality is tested after 12, 14, 48, 72, 96 and 120 hs. exposition to the plant extract

Table 2.4 Examples of biological activities tested in plant extracts

Plant extracts are tested for different biological activities, e.g.: antioxidant, cytotoxic, bactericidal, antimicrobial, insecticidal, etc. (Ciccia et al. 2000; Mongelli et al. 1997; Desmarchelier et al. 1996), etc. (Table 2.4).

Mclaughlin and Rogers (1998) have adopted an interesting approach with four basic assays for starting the analysis of the biological activity of plant extracts. Those assays are: Brine-shrimp (*Artemia salina*) lethality to test *in vivo* lethality in a simple organism, Crown-gall tumors on potato discs to test antitumor compounds, Frond-inhibition of *Lemna* (duckweed) for testing plant growth stimulants and inhibitors, and the Yellow fever mosquito (YFM) test using eggs of *Aedes aegypti* (Linnaeus) for detecting pesticide activity. Other practical protocols can be found in Liu et al. (2013).

Bioassays can be performed *in vitro*, *in vivo* and *ex vivo*. In all cases it is essential to have an appropriate pharmacological model to establish the applicability of any new drug.

The "omics" technologies can also been helpful to predict the pharmacological and toxic profiles and could replace some of the test regularly performed (Ulrich-Merzenich et al. 2007; Buriani et al. 2012; El-Mowafy 2012).

2.5.3.1 In Vitro Assays

They are performed in cells, tissues, microorganisms, insects, mollusks, etc. (Piersen et al. 2004). In general, the approach can be a random screening or a screening based on the traditional knowledge (Agarwal et al. 2014). There is controversy about the extrapolation of *in vitro* results with *in vivo* condition. Several reports have focused on predicting the correlation between both situations (Barnard and Gurevich 2005). In the last years it was suggested as more appropriate a methodology based on system biology or in reverse pharmacology.

2.5.3.2 In Vivo Assays

In vivo assays are accomplished employing laboratory animals as guinea pigs, mice, rabbits, etc. Their use must be limited and respecting the principle of the three "R", Replacement, Reduction, and Refinement, of human-animal experimentation and also considering the legislation of each country (Anonymous 2000; Taylor 2010).

2.5.3.3 Ex Vivo Assays

Ex vivo experimentation is performed in tissues or cells under environmental conditions with minimal alterations respect to the natural environment of the organism of origin. The experimental conditions are more stringently controlled than *in vivo*.

Ex vivo assays are used for testing biological activities such as anticancer activity, estrogenic activity, and anti-clotting activity (e.g.: ecarin clotting time).

2.6 New Technologies

Some of the difficulties related to the discovering of new molecules for treating human diseases are the lengthy and arduous assays required and consequently their implicit costs. New technologies have been developed to facilitate the process. *In silico* predictions gathers data about drug-target interactions available in public databases (Drug-Bank, KEGG Drug, etc.). Connecting that information with human disease networks can contribute with the finding of new drugs for specific pathologies (Nejad et al. 2013; Spiro et al. 2008). Also, genomics, proteomics, transcriptomics, and metabolomics (the omics) contribute to broaden the knowledge about drug-target interactions. Systems Pharmacology profit of those data to elucidate the therapeutic and adverse effects of drugs (Liu et al. 2013; Nejad et al. 2013).

Polypharmacology integrates the existing information about drugs, targets and diseases to design drugs or cocktails of drugs to treat specific disease states with the lowest toxicity. It requires a multidisciplinary approach among computational modeling, synthetic chemistry, *in vitro/in vivo* pharmacological testing, and clinical studies (Reddy and Zhang 2013).

2.7 Concluding Remarks

In the coming years, with the assistance of bioprospecting and ethnobotany, it will be possible to find new medicinal plants still unknown. The holistic approach with *in vivo* and *in vitro* experiments based in chemical and bioassay fractionation will continue contributing to the detection of new compounds (Verpoorte et al. 2006). However, in the last years it became evident that the biological activity of a plant

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extract is, in general, a consequence of the interaction of the active principles of the plant with other plant chemical components, which is not merely the addition of the activities of each plant chemical but a synergistic effect (Lila and Raskin 2005). A multidisciplinary approach with the contribution of the new technologies will gradually have more impact in the identification of plant bioactive principles and associations for their capacity to find out connections between the activities, mode of action, and toxicity of plant extracts.

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Chapter 3 Plant Secondary Metabolism

Abstract Plant metabolism is divided in primary and secondary metabolism according to the functions they display and the characteristics of their biosynthetic pathways. Secondary metabolites are synthesized from primary metabolites and, usually, they are produced within a phylogenetic group, but are not only limited to them.

In general, secondary metabolites display a role in the adaptation of plants to their environment, e.g.: in defense against predators and pests. They are diverse chemical structures broadly classified in three groups: phenolics, terpenes and steroids, and alkaloids. The two first groups have in common an anti-oxidant and anti-inflammatory activity besides the specific biological activities typical of each group. Alkaloids are a heterogeneous group with a variety of actions on the central and peripheral nervous system, among others.

Metabolic engineering has allowed deciphering and modulating some of the metabolic pathways of these metabolites. Also, it is an interesting tool that helps to improve secondary metabolite production of commercial interest. New approaches as systems biology and synthetic biology will help to discover interactions between secondary metabolites and human pathologies and to obtain better secondary metabolite productivities.

Keywords Plant secondary metabolism • Secondary metabolites • Metabolic engineering • Synthetic biology

3.1 Introduction

Plant chemical compounds can be classified as primary or secondary metabolites according to their biosynthetic pathway and functions. The biosynthesis of primary metabolites practically does not differ among the living organisms, playing an essential role for life (growth, metabolism, and reproduction). On the other hand, secondary metabolites are organic molecules not essential for plant growth and development but with important roles in the relationship with the environment as in plant defence and the adaptation of plants to their surroundings (Bernohf 2010; Bourgaud et al. 2001; Harborne 1999).

3.2 Primary and Secondary Metabolism

Plants, and some bacteria, are able to use the solar energy, plus carbon dioxide and water, to synthesize complex molecules (carbohydrates as sucrose and starch) through photosynthesis, a process that generate chemical energy (ATP) to be used in cellular metabolism. Anaerobic and aerobic organisms make use of that chemical energy, with different efficiency, in their specific glycolytic process. In plants, the glucose derived from those carbohydrates produce phosphoenol pyruvate (via glycolysis) and malate (via pentose phosphate shunt).

Secondary metabolites are synthesized from primary metabolites by a sequence of chemical reactions catalyzed by enzymes some of which limits the pathway defining the synthesis and the amount of metabolite produced.

Malate enters into the shikimate pathway to produce tryptophan, from which originate indole alkaloids, and phenylalanine.

Glycolysis take place in the cytoplasm of the plant cell, the obtained phosphoenol pyruvate enters into the mitochondria and in its stroma produces pyruvate, which is transformed into aceto acetyl-CoA. Aceto acetyl-CoA goes into the cycle of the tricarboxylic acid (TCA) in the mitochondrial crests, completing the catabolism of glucose through a series of oxidative reactions, with the production of carbon dioxide and adenosine triphosphate (ATP).

Several molecules, intermediate in the synthesis of secondary metabolites, are produced in the different steps of the TCA, proline that originates pyrrolic alkaloids, fatty acids from which derive phospholipids, triacylglycerol, glycosides, phenols, mevalonate, ornitine, and cinnamic acid. Mevalonate, by a series of intermediate chemical reactions, originates carotenoids, stigmasterol and terpenoids. Orinitine together with phenylalanine (coming from the shikimate pathway) are the precursors of tropane alkaloids, and cinnamic acid originates flavonoids and lignans (Fig. 3.1).

3.3 Secondary Metabolites

Secondary metabolites are diverse chemical structures broadly classified in three groups: phenolics, terpenes and steroids, and alkaloids (Bourgaud et al. 2001; Harborne 1999) (Fig. 3.2). A complex network of transcription factors controls their transcriptional response to developmental or environmental stimuli (Patra et al. 2013; Petinatti Pavarini et al. 2012; Vom Endt et al. 2002). Most of them have an ecological role in regulating the interactions between plants, microorganisms, insects and animals. They often accumulate in the plant in small quantities, frequently in specialized cells, in specific plant developmental steps, or during stress (Piñol and Palazón 1993).

A group of secondary metabolites are high-molecular-weight polymeric compounds such as cellulose, lignanes, etc., which are distributed in all higher plants having mainly a structural function. Others are low-molecular-weight compounds

with a more constrained distribution, in general synthesized in response to the exposition to some biotic or abiotic substances (Dixon 2001). Frequently, they are produced within a phylogenetic group, but they are not only limited to it.

In planta they can be defensive substances, antifeedants, attractants or pheromones. *Ex planta*, they display a variety of biological activities that are exploited by people in different manners (Table 3.1).

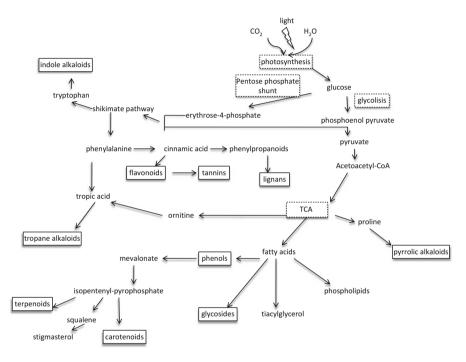


Fig. 3.1 Primary and secondary metabolism in plants

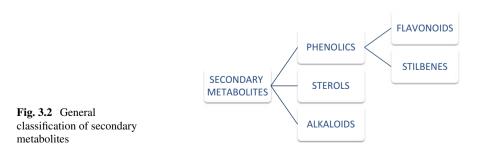


Table 3.1 Plant secondary metabolites with commercial relevance

1. Dyes, flavours and fragrances

Dyes: anthocianins, betacianins, catechu, haematoxylin, gamboge, indigo, rubhada, saffron, madder, weld

Flavours: asparagus, celery, cinnamomum, strawberry, vanilla

Fragrances: cinnamon, capcaicin, eucalyptus, garlic, jasmine, lemon, mint, onion, patchouli, rosewood, sassafras, sandalwood, vetiver. Sweeteners: steviosids, taumatin, miraculin, monellin

2. Agrochemicals

Azadiachtin, dictamine, ecdysterone, harmaline, indanediones, neriifolin, physostigmine, piretrines, polygodial, rotenone, ryanodine, salannin, wyerone

3. Pharmaceuticals

Ajmalicine, artemisinin, atropine, codeine, digoxin, diosgenin, hyoscyamine, L-dopa, morphine, paclitaxel, quinine, scopolamine, serpentine, shikonin, vinblastine, vincristine

3.3.1 Phenolics

Some of the representatives of this group have structural functions (e.g.: lignin reinforcing specialized cell walls). Others participate in plant defense (e.g.: coumarins, condensed tannins, isoflavonoids, proanthocyanidines, stilbenes), pollination, light screening, and seed development.

Chemically, they are characterized as aromatic compounds with one or more acidic hydroxyl groups. Exposed to the air they quickly oxidize and complex with proteins.

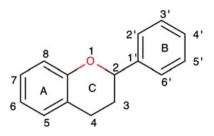
Most phenolic compounds derive from the phenylpropanoid and phenylpropanoid-acetate pathway, being phenylalanine ammonia lyase (PAL) a key enzyme in the pathway. Others derive from alternative pathways, e.g.: tetrahydrocannabinoids are polyketide or terpenoid derivatives. Phenolics are classified in Flavonoids and Stilbens.

3.3.1.1 Flavonoids

Flavonoids are a subgroup of polyphenolic compounds with a characteristic C6–C3–C6 structure. The chemical structure of flavonoids is based on a C15 skeleton bearing a second aromatic ring B in position 2, 3 or 4 (Fig. 3.3). Flavonoids accept several substituents (hydroxyl-, methyl- groups, isopentenyl units, sugars) that are determinants of their solubility. They are a heterogeneous family whose main subclasses are anthocyanidins, flavanones, flavan-3-ols, flavones, flavonols, and isoflavones. Minor groups are aurones, coumarins, chalcones, dihydrochalcones, dihydroflavonols, and flavan-3,4-diol.

They are often located in the vacuole of cells, and are responsible of the color of most of flowers and fruits, functioning as pollinator attractants (pelargonidins, cyanidins, delphinidins), protecting plants from UV-B radiation (kaempferol), or

Fig. 3.3 Chemical structure of flavonoids based on a C15 skeleton



acting as insect-feeding attractants (isoquercetine) or antifeedants (proanthocyanidins). Also, some of them (apigenin and luteoline) participate as signal molecules in the legume-*Rhizobium* association.

Many flavonoids are synthesized by the stimuli of stress as wounding, drought, and exposition to metals and starvation.

Flavonoids, especially flavonols and flavan-3-ols, have been suggested to protect plants from oxidative stress acting as antioxidants (Hernández et al. 2009).

As for their biological activities, they display anti-oxidant function, anti-inflammatory effect (Comalada et al. 2006; Fang et al. 2005), and inhibition of cell-signal proteins (Pang et al. 2006). The Malvidin-3-O-β-glucoside, found in grape, inhibits mediators of macrophage-derived inflammation (Decendit et al. 2013). They were also considered as beneficial against certain types of cancer for their activity, demonstrated by *in vitro* and *in vivo* assays, as modulators of apoptosis, vascularization, cell differentiation, cell proliferation, etc. The cross talk between flavonoids and the key enzymes related to neoplastic cells and metastasis has not yet been elucidated (Batra and Sharma 2013).

3.3.1.2 Stilbenes

They are a small group of phenolic metabolites that participate in plant defense. Resveratrol is the most common stilbene (Fig. 3.4); it could be present as the *cis* or the *trans* isomer and are produced in response to stress (wounding or pathogen attack). *Trans*-resveratrol is the most abundant of both isomers in plant tissues and is considered beneficial against coronary disease in humans for its antioxidant activity (Bradamante et al. 2004). Also, it is though that it has a protective activity against certain kind of cancer (Aggarwal et al. 2004; Kundu and Surh 2008), diabetes (Sharma et al. 2007), and neuro-degenerative diseases (Anekonda 2006; Pearson et al. 2008) through its induction of *Sirtuin-1* genes (Donnez et al. 2006). *Trans*-resveratrol is currently produced from *Polygonum cuspidatum* (syn. *Fallopia japonica*) for being used in health care or from grapevine for cosmetics, among other possible sources (Burns et al. 2002; Counet et al. 2006).

Phytoestrogens are flavonoids with structural similarities to mammalian 17 β-estradiol (E2) (e.g.: resveratrol, genistein, kaempferol, daidzein). They have demonstrated their ability of binding to estrogen receptors (Pilsakova et al. 2010) and,

Fig. 3.4 Chemical structure of resveratrol

Fig. 3.5 Chemical structure of terpenes (a) limonene, (b) menthol

in a similar way as E2, are competent to alleviate postmenopausal complaints, increase bone formation and repress adipose tissue with the advantage of not producing the estrogens induced side effects typical of the hormone replacement therapy (Schilling et al. 2014; Song et al. 2007; Heim et al. 2004).

3.3.2 Terpenes and Steroids

3.3.2.1 Terpenes

They are a group derived from the repetitive "head to tail" (although "head to head" and "head to middle" unions are also possible) fusion of a branched unit of five carbons, the isoprene (Fig. 3.5). They are classified, according to their number of five-carbon units, as hemiterpenes (C1), monoterpenes (C10), sesquiterpenes (C15), diterpenes (C20), triterpenes (C30), tetraterpenes (C40), and polyterpenes (more than 80-carbon units). Plants produce a wide variety of terpenoids in specialized structures such as glandular trichomes, secretory cavities, and glandular epidermis. In general, the C15, C30, and polyterpenes are produced in the cytosol and endoplasmic reticulum (acetate/mevalonate pathway) whereas the isoprene, C10, C20

Terpene	Source	Use
Geraniol	Pelargonium graveolens	Scent
Citral	Cymbopogon flexuosus	Scent
Menthol	Mentha arvensis	Flavour
Camphor	Cinnamomum camphora	Mothproofing treatment
Caryophyllene	Syzygium aromaticum, Cannabis sativa	Spice, anti-inflammatory
Eugenol	Syzygium aromaticum	Spice
Santonin	Artemisia maritima	Anti-parasitic
Artemisinin	Artemisia annua	Anti-malarial
Abietic acid	Pinus spp., Abies spp.	Varnishing, resin soap
Pimaric acid	Pinus spp.	Resin
Stevioside	Stevia rebaudiana	Sweetener
Taxol	Taxus brevifolia	Antitumour activity
Azadirachtin	Azaridachta indica	Insect anti-feedant
Diosgenin solasodine	Dioscorea spp, Solanum eleagnifolim.	Synthesis of steroidal hormones
Digitalis glycosides	Digitalis lanata	Cardiotonic

 Table 3.2 Terpenes of commercial application

and C40 are produced in plastids (glyceraldehyde phosphate/pyruvate pathway) (Croteau et al. 2000). Most of the terpenes have cyclic structures.

Monoterpenes are major components of the aromas of the plants, the essential oils, which are used in perfumery and flavouring industries (Table 3.2).

3.3.2.2 Steroids

Steroids have a cyclopentane perhydrophenanthrene backbone, and derive from tetracyclic terpenes. Ergosterol and stigmasterol are found in the plant kingdom, while some plant steroids, such as the digitalis glycosides (cardenolides) from D. lanata and solasodine from S. eleagnifolium, can be used to synthesize animal steroidal hormones. The most abundant phytosterols are β -sitosterol, campesterol and stigmasterol (95–98 % of all plant sterols) (Fig. 3.6). They have cholesterol-lowering properties and have a protective effect against cardiovascular disease (Sabater-Jara and Pedreño 2013; García-Llatas and Rodríguez-Estrada 2011). Also, they have anti-atherosclerotic, anti-inflammatory and anti-oxidative activities (Delgado-Zamarreño et al. 2009), and antitumor effect against certain types of cancer (Woyengo et al. 2009).

Brassinosteroids are natural plant growth regulators that promote cell expansion and elongation, vascular differentiation, reorientation of microtubules, inhibition of root elongation, and senescence (Bishop and Koncz 2002).

Fig. 3.6 Chemical structure of stigmasterol

Carotenoids provide colour to plants as β -carotene and lycopene that brings their color to carrot and tomato respectively. They are anti-oxidants and precursors in the synthesis of vitamin A.

Saponins are steroidal or triterpenic glycosides some of which were reported as having similar activities as phytoestrogens (e.g.: PNS from *Panax notoginseng*) (Augustin et al. 2011). It was reported that, as phytoestrogens, some saponins are able to influence the balance between osteogenic and adipogenic differentiation of mesenchymal stem cells. In doing so, they would favor or even stimulate osteogenic differentiation, and as a consequence would aid to prevent bone loss and fragility fractures (Schilling et al. 2014). Other saponins, as tigogenin and platycodin, were associated to the prevention of obesity, inhibition of adipogenesis, and promotion of osteogenesis; consequently they are proposed as potentially useful as an alternative treatment in disorders as osteoporosis (Lee et al. 2010; Zhou et al. 2007).

3.3.3 Alkaloids

People have been using alkaloids since centuries, in magical or curative potions, as painkillers, poisons, etc. The use of opium, the latex of *Papaver somniferum* containing codeine and morphine, is already reported in de Middle East as far as 1200–1400 B.C.

Initially, alkaloids were chemically described as basic molecules that contain one or more nitrogen atoms produced by plants (Fig. 3.7). Nowadays it is known that some alkaloids are also produced by certain animals such as the European fire salamander that produces samandarines, frogs and toads that probably overexpress an uptake system for sequestration of dietary arthropod alkaloids into skin glands, or Australian myobatrachid frogs of the genus *Pseudophryne* that synthesize their own unique indolic pseudophrynamines while sequestering pumiliotoxins (PTXs) from a dietary source (Daly et al. 2002).

Alkaloids are molecules capable to form salts with acids and to complex with metal ions. They can be classified based on different characteristics, e.g.: according

Fig. 3.7 Chemical structures of (a) nicotine and (b) caffeine

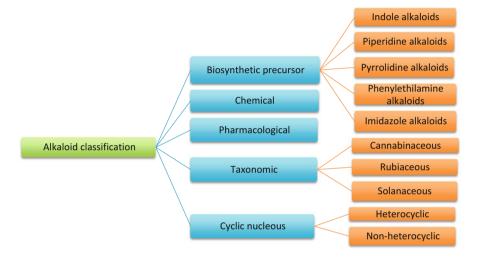


Fig. 3.8 Alkaloid classification according different characteristic and properties

to the aminoacids from which derive, according the structure of the ring system containing the nitrogen atom (pyrrolidine-, indole-, piperidine-, pyrrolizidine-, tropane-, quinoline-, isoquinoline-, aporphine-, imidazole-, diazocin-, purine-, steroidal-, amino-, and diterpene alkaloids), according their pharmacological activities (analgesic, narcotic, etc.), according the taxonomic classification of the plant family where they are mostly found (Cannabinaceous, Rubiaceous, Solanaceous), or the characteristics of the cyclic nucleus (heterocyclic, non-heterocyclic) (Fig. 3.8). About 20 % of plants produce alkaloids; many of them produce more than one type.

The role of alkaloids in plants is mostly in defense against predators as insects (nicotine, caffeine) and herbivores (lupine alkaloids, solasodine), and against microorganisms (berberine, liriodenine) as well. Also, some of them are synthesized in response to tissue damage (nicotine). Quite a lot of them have biological activity (Table 3.3).

Most alkaloids derive from amino-acid precursors (i.e. ornithine, lysine, tyrosine, tryptophan, and histidine) or from anthranilic acid or nicotinic acid. Alkaloid bio-

Alkaloid	Source	Biological activity
Arecoline	Areca catechu	Stimulant
Atropine	Atropa belladonna	Anticholinergic
Berberine	Berberis spp.	Pigment, mild antibiotic
Caffeine	Coffea arabiga	Stimulant
Cocaine	Erythroxylon coca	Anesthesic, stimulant
Coniine	Conium maculatum	Paralysis of nerve endings
Ephedrine	Ephedra sinica	Bronchodilator
Mescaline	Lophophora williamsii	Hallucinogenic
Nicotine	Nicotiana tabacum	Neuroactive, insecticide
Papaverine	Papaver somniferum	Muscle relaxant
Piperine	Piper nigrum	Spice
Quinine	Cinchona ledgeriana	Antimalarial, bitter
Reserpine	Rauwolfia	Antipsychotic
Strichnine	Strychnos	Poison
Theophylline	Camelia sinensis	Stimulant
Vinblastine	Catharanthus roseus	Antineoplasic

Table 3.3 Plant alkaloids with biological activity

synthesis is regulated in time by development and environmental factors controlling the activity of transcriptional factors, which program the whole process. Usually, they are produced in specialized cells, tissues, and organs, where they accumulate or they are transported from the place of synthesis to the place of storage (De Luca and St-Pierre 2000; De Luca and Laflamme 2001).

Catharanthus roseus has been taken as a model system, to elucidate that the biosynthesis of the important anticancer agents vinblastine and vincristine can be regulated by a number of biotic and abiotic stimuli being activated at particular stages of plant development (Shanks and Morgan 1999; Facchini 2001).

3.4 Metabolic Engineering

It was originally defined as 'the direct improvement of production, formation, or cellular properties through the modification of specific biochemical reactions or the introduction of new ones with the use of recombinant DNA technology' (Bailey 1991).

Plant metabolic engineering plays a special role in biotechnological approaches for covering the escalating demands of food, energy and medicines of an evergrowing world population (Dudareva and DellaPenna 2013).

Genetic engineering of secondary metabolite biosynthesis is intended to increase the amount of a compound of interest or decrease the amount an unwanted metabolite in plants. To increase the amount of a specific metabolite, or to incorporate the synthesis of novel compounds, the inhibition of competitive pathways, the reduction of the catabolism of the target compound, and the modification of the expression (over expression or suppression) of regulatory genes are approaches that have been explored. On the other hand, to reduce the amount of an undesirable compound the approach can be the knock out of a certain enzymatic step by RNA antisense, RNA co-suppression or RNA interference, or the over expression of an antibody against any key enzyme in the pathway. Also, diverting the pathway into a competitive one, or increasing the catabolism of the undesired product has been used (Verpoorte and Memelick 2002). Even though plant metabolic engineering has had some success the modifications of chemical profiles is complex and mostly an ineffective strategy (Jirschitzka et al. 2013).

Up to date, the best-studied pathway at genetic level is that from flavonoids and anthocyanins. Also, there are great advances in the elucidation of the indole and isoquinoline alkaloid pathways (Allen et al. 2004; Runguphan and O'Connor 2009; Glenn et al. 2011; Park et al. 2003).

In plants, transcription factors (TF) regulate the expression of multiple genes in a single biosynthetic pathway. TFs from the biosynthesis of defense compounds are mainly from the bZIP, MYB, MYC, WRKY and ERF families. In the case of anthocyanin and tannin pathways, MYB family transcription factors are fundamental for the coordinated activation of genes (Dixon et al. 2013). Jirschitzka et al. (2013) summarize the TFs that were lately employed in the engineering of plant defence pathways and that were used to manipulate the biosynthesis of e.g.: proanthocyanidin in poplar, artemisinin in *A. annua*, nicotiana in *N. tabacum*, sesquiterpenes in *A. thaliana* (Hong et al. 2012), terpenoid indole alkaloid in *C. roseus* (Suttipanta et al. 2011). What is more, TFs from a species have demonstrated to be effective in regulating the biosynthetic pathway in other species; e.g. AtMYB12 from *A. thaliana* also increases the concentration of phenylpropanoids and flavonoids in *N. tabacum* (Misra et al. 2010).

A limitation on the use of transcription factors is their possible effects on multiple pathways that could lead to unwanted phenotypes.

Multigene engineering (Christou 2013) has also helped to the development of crops with more complex traits, including extended metabolic pathways producing valuable compounds such as β -carotene in Golden Rice (Ye et al. 2000) and three different vitamins (β -carotene, ascorbate, and folate) representing three different metabolic pathways in Multivitamin Corn (Naqvi et al. 2009).

When engineering a metabolic pathway, promoters have also to be considered. Certain compounds are only produced in specific organs, tissues, or specific storage structures because it is the site of accumulation of their precursors, because in that place they are less susceptible to degradation, or plant tissues are protected from their toxicity. Selecting the adequated promoter is thus fundamental for the expression of the involved genes. In the case of multigene constructs, genes can be under the same promoter (Moldrup et al. 2012; Geu-Flores et al. 2009a) or each gene can have a different promoter (Farhi et al 2011). Also, constitutive (Samac et al. 2004) or organ-specific promoters can be used (Redillas et al. 2012; Bai et al. 2011), being the last strategy more adequate for avoiding spurious side products, to improve yield, avoid autotoxicity, and increase crop protection.

A typical example is the biosynthesis of monoterpene indole alkaloids in *C. roseus* (Heinig et al. 2013) where the metabolism takes place across various

cellular locations, including the chloroplast, vacuole, nucleus, endoplasmic reticulum, and cytosol (Verma et al. 2012). Thus, when engineering a particular biosynthetic pathway it is important to take into account this information because the ignorance of which specific enzyme participates at a defined localization can be determinant of the failure.

Data mining is today a prerequisite to a successful strategy (Giddings et al. 2011; Hagel and Facchini 2010; Winzer et al. 2012; Liscombe et al. 2010). Bioinformatics play a remarkable role in offering all the information needed about co-expression analyses, comparative metabolite profiling, transcription factors and enzymes at metabolic bottlenecks.

To perform gene-stacking, RNA-based silencing systems, including RNAi (Runguphan et al. 2009), the use of synthetic RNA elements, ribosome binding site elements, and a combination of promoters strategically placed in front of stacked pathway genes could hypothetically facilitate to modulate protein expression (Hawkins and Smolke 2008; Chang et al. 2012; Glenn et al. 2013).

The intrusion in the secondary metabolite to favor the biosynthesis of a particular compound has to take into account not to deplete the primary metabolism.

3.5 Synthetic Biology

The main goal of synthetic biology is to modify a biosynthetic pathway in an organism in order to increase or produce a specific compound (Kliebenstein 2014). The establishment of multigene/protein-based networks has enabled the construction of novel synthetic pathways (Purnick and Weiss 2009). The integration of multiple genes involved in a metabolic pathway into a single vector under different promoters was already used for producing carotenoids, vitamin E and PUFAs (Naqvi et al. 2010), glucosinolates (Geu-Flores et al. 2009b) and artemisinin (Farhi et al. 2011).

The fact that some secondary metabolites are stored in different sites than those of biosynthesis necessitates intracellular and intercellular transport. However, there are only very few reports about transport engineering in synthetic biology (Goossens et al. 2003), possibly due to the limited molecular knowledge on intracellular transport and cellular excretion of specialized metabolites (Nour-Eldin and Halkier 2013). Glucosinolates are an excellent model system for studying transport of specialized metabolites (Nour-Eldin and Halkier 2009).

3.6 Systems Biology

Systems biology is about the data integration and the use of the omics technologies to understand the cell at a system level (Noble 2008; Sagt 2013). Also, it considers a biological system feasible to be modeled as a network (Bebek et al. 2012). Network analysis can be classified in: omics data modeling (stoichiometric modelling, kinetic modeling), which is the use of statistical methods to identify and infer complex

functional interactions among the components in biological systems (Chae et al. 2012), stoichiometric modelling which predicts flux distributions of biological pathways (Schellenberger et al. 2011), and kinetic modeling, which is utilized for the evaluation of the dynamics of biological systems such as time-course simulation, steady-state analysis and metabolic control analysis (Rohwer 2012). From them, omics data modeling is the most commonly used for predicting gene function and comprehend a whole biological system, allowing the elucidation of various networks as metabolite-to-metabolite, gene-to-metabolite and protein-protein interactions (Vidal et al. 2011) (Yonekura-Sakakibara et al. 2013). The combination of plant metabolomics, plant systems biology, and bioinformatics has generated and assembled enough data to model complex plant processes (Christou 2013).

The methods of Network flux analysis (NFA) differ from one another in the size and complexity of the network under analysis and in other factors as the type of information, insight and predictions they make (Shachar-Hill 2013). Plant metabolic networks are more complicated and numerous, with the additional factor that they have several metabolic flux options in a pathway or among the different cells of a specific organ in a determined step of plant development. A good example of NFA application in plant metabolism is the dynamic modeling of monoterpene biosynthesis in peppermint. The hypothesis of an undiscovered regulatory inhibition of a key enzyme was tested *in silico* and *in vitro* finding a good agreement between the simulated and experimental monoterpene accumulation profiles and feedback inhibition (Rios-Estepa et al. 2008).

3.7 Conclusive Remarks

The plant kingdom has a great proportion of species yet unknown or whose chemical composition has not been described. Secondary metabolites display a diverse set of biological activities of therapeutic use; the finding of new plant species or plant compounds could increase that battery of chemicals for fighting diseases. The production at large-scale of secondary metabolites can be improved by optimization the process of production, harvest and down-stream processing of metabolites from crops or by using the technology of production in *in vitro* cultures (phytofermentations). Combining those strategies with the new approaches of systems and synthetic biology will help to discover interactions between drugs and pathologies and to obtain better productivities.

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Chapter 4 In Vitro Plant Cultures as Biofactories

Abstract *In vitro* plant cell cultures are defined as a culture in aseptic conditions of any part of the plant body in a nutritive media. Cells, differentiated and undifferentiated (calli and suspended cells) tissues, and organs can be maintained *in vitro*.

Some of the advantages of *in vitro* cultures are their development and maintenance in defined conditions (nutrients, light, humidity, temperature), independent from environmental influences (pests, diseases, extreme weather, geographical location, etc.), and manipulated by experienced operators in confined facilities.

Since its development, *in vitro* plant cell cultures have been an essential tool for studying plant metabolism, and to micropropagate plant species, maintaining their genetic background. Also, they were helpful to analyze and optimize the production of plant secondary metabolites.

Secondary metabolites productive processes are conducted, with a different degree of success, in undifferentiated cultures and in cultures of transformed organs. Several strategies were displayed in order to increase yields as manipulation of the plant growth regulator balance, addition of precursors, biotransformation, and immobilization.

Also, as plant cells have a different behavior in liquid culture compared with microorganisms and mammal cells, bioreactor design was adapted to develop plant cell cultures.

Keywords *In vitro* plant cell cultures-plan growth regulators • Culture mediaelicitation • Undifferentiated cultures-hairy roots-scaling up

4.1 Introduction

In vitro plant cultures can be defined as the culture, in aseptic conditions, of cells, tissues, organs, and plants under definite physical and chemical conditions, in a vessel. The first report of an *in vitro* plant cell culture dates from the early twentieth century, when Haberlandt cultured single palisade cells from leaves in Knop's salt solution plus sucrose (Haberlandt 1902).

The first commercial interest on plant tissue cultures was to propagate ornamental and food species (Pacheco et al. 2012; Gonçalves and Romano 2013; Rout et al. 2000; Mulder-Krieger et al. 1988). By the end of the 1970s, on the basis of the

previous experience with microbial fermentations, the interest on *in vitro* plant cell cultures for producing plant metabolites escalated.

Since the 1980s, *in vitro* cultures became an important tool in basic and applied studies generating knowledge on plant metabolism and on the optimization of productive processes of metabolites in plant cells (phytofermentations).

In a first period, research was mainly focused on the production of plant natural products by *in vitro* cultures of a specific species. In a second period, the advances in genetic engineering, bioengineering, plant physiology, and the development of new areas, as metabolic engineering and molecular farming, increased the interest on plant tissue cultures for producing novel or heterologous compounds (e.g.: recombinant proteins).

Chapter 6 of this book describes the application of *in vitro* cultures for molecular farming, which is the production of heterologous proteins of commercial interest in GMOs as transgenic plants. In this chapter the focus will be on the contribution of *in vitro* plant cell cultures to the production of secondary metabolites.

4.2 In Vitro Cultures for Producing Secondary Metabolites

Chapter 3 covers plant secondary metabolism and the biological activities secondary metabolites display as their participation in defence against herbivores (insects, molluscs, vertebrates), and microorganisms (virus, bacteria, fungi), and their metabolic and ecological functions (attracting pollinators, animals that spread seeds, UV protection) (Wink 1988; Wink et al. 2005).

In vitro cultures are feasible due to the totipotency of plant cells, which is the capability of most of plant cells to regenerate a whole plant, identical to the parental plant, when exposed to the adequate conditions. Totipotentiality is also physiologically, which means that plant cells bear the essential genetic information for producing the same secondary metabolite pattern of the source plant.

In vitro plant cell cultures have been successfully used for producing natural secondary metabolites at laboratory scale (Table 4.1). The main advantages of *in vitro* cultures are the development of cultures in environmental controlled conditions, independent of the weather, quality of the soil, seasonality, and day-length, free from mycotoxins, herbicides or pesticides, and in relatively small facilities (Ramachandra Rao and Ravishankar 2002).

Basically, *in vitro* plant cell cultures are developed placing a piece of plant tissue, the explant (leave, stem, etc.), previously sterilized, on the surface of a nutritive medium contained in a vessel (Petri dish, flask, etc.). The nutritive medium usually contains macronutrients, micronutrients, vitamins, myo-inositol, a source of carbon (e.g.: sucrose), plant growth regulators and, if it is a semi-solid culture, a solidifying agent, usually agar. Several culture media were developed (Murashige and Skoog 1962; Gamborg et al. 1968; Schenk and Hildebrandt 1972), which are the base of almost all the culture mediums in use. Each plant species and even each duple plantmetabolite needs a culture medium with a specific composition.

 Table 4.1 Secondary metabolites from in vitro plant cell cultures

Plant species	Secondary metabolite	Activity	Reference
Lavandula viridis Her	3-O-caffeoylquinic, 4-O-caffeoylquinic, 5-O-caffeoylquinic, rosmarinic acids, luteolin and pinocembrin	Antioxidant, anti-cholinesterase	Costa et al. (2013)
Ocium basilicum	β-caryophyllene, essential oils	Antiviral, antioxidant, antibacterial. Aroma	Bertoli et al. (2013)
Cistus creticus subsp. creticus	Labdane diterpenes	Antibacterial, cytotoxic	Skoric et al. (2012)
Valeriana glechomifolia	Valepotriates	Mild sedative	Russowski et al. (2013)
Larrea divaricata	Nordihydroguaiaretic acid	Antioxidant, inhibitors of lipoxygenases	Palacio et al. (2012)
Vitis vinifera	Anthocyanins	Antioxidant	Nagamori et al. (2001)
Salvia spp.	Terpenoids, polyhenols	Antioxidant, antimicrobial, anti-inflammatory, anti-carcinogenic	Marchev et al. (2013)
<i>Berberis buxifolia</i> Lam	Berberine	Anti-bacterial, anti-diarrheal, antispasmodic	Alvarez et al. (2009)
Silybium marianum (L.)	Silymarin	Anti-inflammatory, antioxidant, anti-carcinogenic	Sánchez- Sampedro et al. (2008)
Stevia rebaudiana Bertoni	Steviosides	Sweetener	Rajasekaran et al. (2008)
Hypericum perforatum L.	Hypericin, pseudohypericin and hyperforin	Treatment of neurological disorders and depression	Zobayed et al. (2003)
Glycyrrhiza glabra	Flavonoids	Anti-microbial	Li et al. (1998)
Panax ginseng	Ginsenosides	Anti-oxidant	Huang et al. (2013a), Huang et al. (2013b)
Thalictrum minus	Berberine	Anti-bacterial, anti-diarrheal, antispasmodic	Kobayashi et al. (1988)
Papaver somniferum	Sanguinarine	Anti-carcinogenic, antimicrobial	Park et al. (1990)

Cultures are then placed in favorable conditions (temperature, light, photoperiod, irradiance, humidity) for growth and for producing the metabolite of interest. That requires a deep analysis and optimization of the best conditions for optimal growth and production. Sometimes cultures are developed in two-steps, in the first step in a

condition that favors growth and in a second step in a condition that favors metabolite production (Alvarez et al. 2009).

In a conventional approach, the development of *in vitro* plant cell cultures for producing secondary metabolites has two main stages. The first one is related to the establishment and maintenance of the *in vitro* culture. This phase involves the optimization of the conditions of culture (culture media composition, light, darkness, temperature, etc.), and the maintenance of the culture viability during the successive subcultures to fresh media. Usually, during this first step emerges the somaclonal variation, characteristic of in vitro cultures that imply a collection of genetic and epigenetic changes, frequently in a higher frequency than those expected in nature. That variation appears as soon as the tissues are separated from the parental plant and placed in culture. The cell proliferation produces a heterogeneous cell population, at a morphological, genetic, molecular and biochemical level, and increases with the time in culture. Thus, it is essential to perform a constant screening and selection of the producing lines (Wang and Wang 2012). If this aspect of in vitro cultures is neglected, the attempts to maintain high stable yields are often frustrated. The second stage is the optimization of the conditions for increasing yields and the scaling up to a bioreactor at laboratory and pilot plant scale.

4.3 Establishment and Maintenance of *In Vitro* Cultures

The selection of the plant material for starting *in vitro* cultures is the first step of the process. Explants can be any part of the plant body but in general the most used are pieces of leaves and stems, as they provide the highest amount of biomass (Nigra et al. 1987). They are heterogeneous and contain different cell types, which produce a heterogeneous cell population that differ in rates of growth, ploidy level, physiology, etc. It was demonstrated that the biosynthetic capacity of the explants source influences the yield of the *in vitro* culture. High producing parental plants often originated high producing *in vitro* cell cultures. However, variations were demonstrated among cultures from the same parental plant, e.g., *Ruta graveolens* stemderived explants produced stem specific essential oils while those derived from roots produce root specific essential oils. Hence, the isoenzyme pattern varies among suspension cultures derived from root, cotyledon and hypocotyl (Arnison and Boll 1975). So, in some cases, the parental plant can have a significant influence on the variation of the biosynthetic activity of cultures through the heterogeneity of the explants. In other cases, the metabolite production is not related to the explant.

Once established the best starting material (explant), the focus is the establishment and maintenance of the undifferentiated cultures (calli) through the optimization of the culture conditions. The classical aspects to analyze are the environmental conditions: composition of the culture medium (inorganic compounds, iron source, vitamins, carbon and nitrogen sources, plant growth regulators), and variables as illumination, temperature, etc. The different variables are tested following a statistical design (Mize and Chun 1988).

Growth is determined by standard techniques (fresh weight, dry weight, index growth) (Ryu et al. 1990), and metabolite content with specific analytical methodologies (colorimetric, HPLC, GC, ELISA, etc.).

Once established, calli are maintained in the optimized conditions and subcultured into fresh culture medium periodically, the optimal time for transfer varies in each case. In general, samples are taken in each subculture and used to determine the variables of growth and metabolite production. It is said that different chemotypes co-habit in the tissue (Sivanandhan et al. 2013), so repetitive selection of the most productive cells is fundamental to avoid the overgrowth of less- producing cells and for establishing productive cultures (Georgiev et al. 2006; Wallaart et al. 2000).

Once performed the screening and selection of the productive lines, calli are employed for starting suspension cell cultures, which are the most convenient systems for conducting a productive process at large-scale. Cell suspension cultures are started transferring friable calli to Erlenmeyer flasks containing a culture medium of the same composition of the solid culture medium but without the gelling agent. In general, in this step factors as inoculum age and size, and concentration of some culture media components (e.g.: plant growth regulators, precursors, etc.) have to be optimized. Then, the cell suspension cultures have to be characterized in their parameters of growth and metabolite production. Growth can be measured by fresh and dry weight, packed cell volume, cell number, cell viability, medium conductivity, and/or protein and/or DNA content (Madhusudhan et al. 1995; Grant and Fuller 1971; Yeoman and Mitchell 1970; Lowry et al. 1951). Metabolites are measured as in calli.

4.4 Strategies to Improve Secondary Metabolite Production

In general, secondary metabolite yield in *in vitro* cultures is low. After establishing the profile of growth and production of the metabolite of interest, the following phase is the optimization of the conditions for achieving the highest yields. Various physical and chemical factors influences *in vitro* cultures, as pH, temperature, aeration, agitation, light, composition of the culture medium including plant growth regulators, addition of precursors and/or elicitors, systems of culture (immobilized cells, undifferentiated or differentiated cultures), process operation (batch, fedbatch, continuous culture), etc. (Benlarbi et al. 2014; Malik et al. 2011).

4.4.1 Age and Inoculum Size

The age of the inoculum is a key factor as the production of the secondary metabolite is sensitive to the physiological age of the inoculated cells (Parsons et al. 2001). Also, the size of the inoculum is significant, the amount of cells that are inoculated in fresh media in every sub-culture affects the rate of growth as well as the

secondary metabolite accumulation rate and final yield (Parsons et al. 2001; Zenk et al. 1977). In general, lowering the density of cells inoculated increases the specific rate of growth and the speed of synthesis and decreases the final yield.

4.4.2 Culture Media Composition

The media composition (carbon, nitrogen, phosphorus and potassium sources) affects both the primary as the secondary metabolism (Nigra et al. 1989; Shinde et al. 2009; Karwasara and Dixit 2012).

Essential elements of culture media are the macroelements, nitrogen, phosphorus, potassium, calcium, magnesium and sulphurum; the microelements iron, manganese, zinc, boron, copper, molybdenum, a carbon source (sucrose, glucose, lactose, maltose, starch); vitamins, myo-inositol and PGR.

It was established that, in general, there is a reverse relationship between cell growth and product yield with a tendency of the secondary metabolites to accumulate in the later phase of growth. Thus, one of the proposed strategies is restraining growth by limiting the carbon, nitrogen or phosphorus sources.

Other components of the culture media can also be modified in order to increase yields. For example, cell suspension cultures of *Silybum marianum* (L.) Gaertn were grown in a Murashige and Skoog calcium- free culture medium resulting in an increase of silymarin accumulation. A paradoxical case is that the production of isoflavonoids by soybean cultures decreased by removing calcium from the culture medium (Stäb and Ebel 1987).

Table 4.2 shows the components of the Murashige and Skoog medium, which is one of the most used in *in vitro* cultures.

4.4.3 Plant Growth Regulators (PGR)

PGR have a remarkable influence on cell growth and secondary metabolite. While primary metabolism brings the energy and the structural units for plant life, PGR regulate the rate of growth of each individual part and integrates them in the

Group	Components	
Major inorganic nutrients	NH ₄ NO ₃ , KNO ₃ , CaCl ₂ .2H ₂ O, MgSO ₄ .7H ₂ O, KH ₂ PO ₄	
Trace elements	KI, H ₃ BO ₃ , MnSO ₄ .4H ₂ O, ZnSO ₄ .7H ₂ O, Na ₂ MoO ₄ .2H ₂ O, CuSO ₄ .5H ₂ O, CoCl ₂ .6H ₂ O	
Iron source	FeSO ₄ .7H ₂ O, Na ₂ EDTA.2H ₂ O	
Vitamins	Myo-inositol, nicotinic acid, pyridoxine-HCl, thiamine-HCl, glycine	
Carbon source	Sucrose	

Table 4.2 Murashige and Skoog media components (Murashige and Skoog 1962)

whole plant. In general, PGR are plant-organic compounds that influence physiological processes at low concentrations. Those processes are growth, differentiation and development. Other processes, as stomata movement, can be affected by PGR as well. PGR are in general into one of the following groups: auxins, cytokinins, gibberellins, ethylene, abscisic acid, and jasmonic acid. From them, auxins and cytokinins play an important role in *in vitro* cultures. It is well known that the relationship auxins: cytokinins induce calli development and also plant regeneration from calli. Additionally, they have a great influence on secondary metabolite production (Muthaiya et al. 2013).

The prototype of auxins is the indole acetic-3-acid (IAA), which is a natural PGR that can be found conjugated to aspartic acid. IAA precursors can also have auxin activity (e.g.: indole acetic aldehyde), and also other components as phenyl acetic acid.

In general, auxins promote cell growth and elongation. In *in vitro* cultures, they induce cell division, cell elongation, formation of adventitious roots, and inhibition of adventitious and axillary shoot formation, induction of embryogenesis, callus initiation and growth. Synthetic auxins as 2,4- dichlorophenoxyacetic acid (2,4-D), naphthalene acetic acid (NAA) and indole butyric acid (IBA) are frequently used for their chemical stability (Morini et al. 2000).

Other compounds in use that are not chemical related to auxins but display the same activity are 3,6-dochloro-o-anysic acid (DICAMBA), 4-amino-3,5,6-trichloropiridine-2-carboxylic acid (PICLORAM) which at high concentrations are herbicides. There are a great number of reports related to the influence of auxins on calli initiation (Nigra et al. 1987; Ahmad et al. 2010).

Sometimes, *in vitro* cultures loss, in an inheritable form, their need of auxins, a phenomenon known as habituation (Kevers et al. 1996).

Auxins are generally used at a concentration range of $0.01-10.0 \text{ mg } l^{-1}$.

Cytokinins (CK) derive from adenine and can be present as a riboside or ribotide. They are characterized for their ability of inducing cell division in combination with auxins. The most common natural cytokinin is zeatine. In *in vitro* cultures the most used are kinetine and zeatine (Aremu et al. 2013). Also benzyl-aminopurine (BAP), a synthetic cytokinin, is used. BAP induces adventitious shoots in *Larrea divaricata* and *Echinacea angustifolia* D.C. (Palacios et al. 2012; Lucchesini et al. 2009).

Cytoquinins regulate cell division, stimulate auxiliary and adventitious shoot proliferation, differentiation, and inhibit root formation. Also, they activate RNA synthesis.

In general cytokinins are used in *in vitro* cultures in the presence of auxins. When only a cytoquinin is needed it is assumed that the cells are producing their own auxins (Flick et al. 1983).

In *in vitro* cultures cytoquinins are used at a concentration range of $0.01-10.0 \text{ mg } l^{-1}$.

The abscisic acid (ABA) is a PGR synthesized from mevalonic acid in mature leaves, mainly in response to hydric stress. Seeds are also rich in ABA. In somatic embryogenesis, ABA can prevent early germination allowing a better embryonic development. It was demonstrated that ABA participates in the response to abiotic

stress through the stimulus of stomatal closure, desiccation tolerance and dormancy induction in seeds. ABA is occasionally used to postpone growth and to moderate the effect of auxins and cytokinins. In plant tissue cultures ABA is used as inhibitor of plant growth for slow-growth conservation, anti-transpirant during plant acclimatization and to induce maturation or the quiescent state in somatic embryos, among other activities (Rai et al. 2011; Prakash and Gurumurthi 2010; Vahdati et al. 2008; Shiota and Kamada 2008). Also, ABA displays a protective effect against cytokinin-induced programmed cell death (apoptosis) (Carimi et al. 2003). ABA synthesis is inhibited by fluridone.

Gibberellins (GA) are a family of compounds (more than 90) based in the structure of the *ent*-giberellane. The most widely distributed GA is the gibberelic acid (GA3), which is produced by fungi. In plants the most significant is GA1 responsible of stem elongation. However, GA utilization in *in vitro* cultures is not widely distributed. It was demonstrated that the addition of GA3 affects calli expansion, viability, stem and roots regeneration, etc. On the contrary, in cell suspension cultures sensibility to GA3 is related to the number of cell divisions after the stationary phase, the duration of the lag phase in cultures with low inocula density, and to the secretion of amilase, peroxidase, phenolic compounds and pectinic acid. In *in vitro* cultures of *Datura inoxia* and *Brugmansia candida* hairy roots, GA3 promotes the increase of fresh weight, elongation and formation of lateral branches. Although cell suspension cultures are generally not responsive to GA3, certain species of *Spinacia* and *Rosa* are sensitive (Randoux et al. 2012; Dalton and Street 1976). Paclobutrazol, ancymidol, and other similar compounds inhibit gibberellins synthesis.

It is not possible to generalize about the type and quantity of PGR adequate for developing a productive *in vitro* culture; a case-by-case analysis has to be performed. However, there is an immense literature on the subject. Some examples are the production of vincristine and vinblastine by *C. roseus* (Scragg et al. 1989; Zhao et al. 2009; Taha et al. 2009; Verma et al. 2013), ajmalicine by *Rauwolfia serpentina* (Zenk et al. 1977; Goel et al. 2009; Susila et al. 2013), berberine by *Berberis buxifolia* or *Thalictrum* sp. (Alvarez et al. 2009; Smolko and Peretti 1994; Kim et al. 1990; Suzuki et al. 1988; Nakagawa et al. 1984), etc.

Other strategies to increase secondary metabolite production have also been effective (Sharma et al. 2011) as the removal and addition of precursors, differentiation and compartmentation, elicitation, immobilization, biotransformation, and transformed cultures.

4.4.4 Removal and Addition or Precursors

The removal of end products is attempted to eliminate its inhibitory effect. The beneficial effect of this approach was demonstrated by the increase in ajmalicine content following the addition of a resin enclosed in porous Miracloth to *C. roseus* suspensions (Wong et al. 2004). The addition of precursors or intermediates, whose

Secondary metabolite	Cell line	Productivity (g l ⁻¹ d ⁻¹)	Reference
Anthocyanin	Vitis (Bailey Alicant A), Vitis (hybrid)	0.06	Yamakawa et al. (1983)
Berberine	Thalictrum minus	0.05	Kobayashi et al. (1988)
	Coptis japonica	0.60	Fujita (1988)
		0.1	Hussain et al. (2012)
Diosgenine	Dioscorea spp.	0.75	Fowler and Scragg (1988)
Rosmarinic acid	Coleus blumei	0.91	Ulbrich et al. (1985)
Sanguinarine	Papaver somniferum	0.034	Park et al. (1992)
Shikonine	Lithospermum erythrorizon	0.15	Tabata and Fujita (1985)

Table 4.3 Productivity of secondary metabolites of commercial interest produced in plant *cell in vitro* culture

influence diminishes with the number of intermediate steps between them and the end product, have been effective in certain cases. In some situations, supplementing endogen or exogen precursors can increase the *in vivo* enzymatic activity. In most of the *in vitro* cultures, however, even in optimal conditions, the biosynthetic rate of secondary metabolites remains low due to the limited expression of the genes for the enzymes of the secondary metabolism (Table 4.3).

The production of the cytotoxic lignan nordihydroguaiaretic acid (NDGA) and the phenylpropanoids p-coumaric acid, ferulic acid and sinapyl alcohol, and cell growth were analyzed in *L. divaricata* Cav. plant cell cultures after the addition of the precursors L-phenylalanine, cinnamic acid, ferulic acid, and sinapic acid. Only the addition of L-phenylalanine (0.5, 1.0, 3.0 mM) resulted in an increase of NDGA and p-coumaric acid. On the contrary, increasing levels of L-phenylalanine resulted in a diminution of the bioconversion into sinapyl alcohol. Cinnamic acid at low concentrations (0.5 mM) only stimulated growth, whereas cinnamic acid at higher concentrations (1.0 and 1.5 mM) and ferulic and sinapic acid at all the concentrations tested resulted toxic to the cell (Palacio et al. 2011).

4.4.5 Elicitation

The addition of elicitors, triggers the accumulation of phytoalexines (Patel and Krishnamurthy 2013; Cusido et al. 2014). Elicitors can be abiotic (heavy metal salts, UV radiation, chemicals with high affinity to DNA or that disrupt the cell membrane) or biotic (structural polysaccharides of e.g.: fungi mycelia wall) (Savitha et al. 2006; Antognoni et al. 2007; Wiktorowska et al. 2010; Cai et al. 2011; Bertoli et al. 2013).

The production of ginsenoside by suspension cultures of *Panax ginseng* was elicited by vanadate, added at the 4th day of culture at a concentration of 50 μ M. In this case, the elicitation was mediated by jasmonic acid (JA) and the transcriptional

levels of genes that codify for key enzymes in the biosynthesis (sqs, se and ds) were increased (Huang and Zhong 2013). The same research group demonstrated that the H⁺-ATPase inhibitor N,N'-dicyclohexylcarbodiimide (DCCD) was an effective abiotic elicitor that triggers the NO-mediated signal transduction pathway, with an increase in the sqs, se, and ds gene expression, and as a consequence an enhanced production of ginsenosides (Huang et al. 2013a).

Methyl jasmonate also elicited by 5–6 times the production of isoflavonoids by *Glycine max* plant cell suspension batch culture (Gueven and Knorr 2010).

An interesting example of elicitation is the effect of salicylic acid combined with ultrasound on the production of valepotriates by *Valeriana glechomifolia* plants growing in liquid medium. Each elicitor improved independently the valepotriates content almost 2-times, the first one causing a slight inhibition of growth depending on the concentration and time of exposition to the elicitor, the second one not affecting growth in any of the conditions tested. Conversely, salicylic acid did not modify valepotriates content in *V. glechomifolia* roots, maybe because in roots the biosynthesis of valepotriates is not through a salicylic-independent pathway (Russowski et al. 2013).

The effect of ultrasound eliciting the biosynthesis of secondary metabolites in cultures in liquid medium can be explained by the induction of hydrodynamic events that cause shear stress to plant cells, which trigger a defense-responding activation of genes. Ultrasound resulted also beneficial for the accumulation of Taxol® by *Taxus chinensis* (Wu and Ge 2004).

The combined effect of JA and β -cyclodextrins (β -CD) was also demonstrated to elicit the production of phytosterols by cell suspension cultures of *Daucus carota*. The β -CD combines a promoter effect of the remotion of product from the culture medium with an inductor effect on metabolite biosynthesis, which is enhanced by JA (Sabater-Jara and Pedreño 2013).

Another elicitation strategy is the addition of fungal extracts to culture media. Pérez et al. (2001) have increased peroxidase amount in hairy root cultures of *Armoracia lapathifolia* by the addition of extracts of fungal plant pathogens (*Colletotricum graminicola, Fusarium moniliforme, Phomopsis, F. solani, N. vasinfecta, P. acanthicum, Pythium, and Phoma medicaginis* var. pinodella).

4.4.6 Differentiation and Compartmentation

The accumulation of secondary metabolites can be according two different patterns related to plant growth and development: (a) they accumulate during the stationary growth phase or associated to differentiation, as is the case of the anthocyanines produced by *V. vinifera* cultures; (b) accumulation during the exponential growth phase, as is the case of isoflavonoids by soy plant callus suspension culture (Gueven and Knorr 2010). The second case is the most frequent because plants need a certain degree of differentiation for the synthesis of determined secondary metabolites.

Although the biosynthesis of a secondary metabolite can take place in all the tissues and cells of the plant, usually the synthesis of some metabolites is restricted to specific tissues and even to specific cells (Nigra et al. 1989; Luckner 1990). That can be associated to a lack of expression of genes that control essential pathway steps in non-specialized cells, a deviation of substrates form the biochemical pathway, an inoperability of the transport mechanisms that allow the removal of potentially toxic end products, the unavailability of secondary metabolites characteristics storage sites, and the catabolic deregulation of the synthesized product. Therefore, the lack of secondary metabolites could be the consequence of an incorrect or absent cell specialization. Frequently, the differentiation of undifferentiated tissues produces a partial or complete restoration of the capacity of accumulating secondary metabolites. Although the production of secondary metabolites in regenerated organs (adventitious stem and roots) via the manipulation of the PGR relationship was broadly studied, the most remarkable results were obtained after the development of the technology of plant transformation.

Also, cell compartmentation has also to be considered. Some molecules are produced in the cytoplasm, while others are produced in chloroplasts, mitochondria, or the endoplasmic reticulum. The formation of ginsenosides in *in vitro* cells of *Panax japonicus* var. repens is proposed to be closely related to compartmentation since the accumulation of the PPD-type ginsenosides is strongly dependent on malonylation that targets them to the vacuoles (Kochkin et al. 2013).

Precursors and intermediate molecules are compartmentalized and driven to specific metabolic steps. *In vivo*, most of the enzymes from the secondary metabolism work in limiting conditions of substrate and do not achieve their maximal rate (Sakuta and Komamine 1987).

Secondary metabolites can accumulate in the place of synthesis or can be transported to other tissues or plant organs. In some cases their production is restricted to a specific development stage (e.g.: flowers, fruits, plantlets, etc.) or to ecological or environmental conditions (e.g.: phytoalexins after a wound or microbial attack).

One of the disadvantages of *in vitro* plant cell cultures is their low growth, fragility and genetic instability that demand a continual selection of producing lines. According to their productive capacity of secondary metabolites, *in vitro* plant cell cultures can be classified into four categories: (a) cultures that always produce the compound (*Morinda*, *Galium*, producers of antraquinones), (b) cultures with producing cells in presence of a majority of non-producing cells (*Catharanthus*, *Solanum*, producers of ajmalicine and solasodine respectively), (c) cultures that usually do not produce the compounds that the parental plant produces (*Papaver somniferum*, *Datura*, producers of morphine and scopolamine respectively), and (d) cultures that produce compounds that are not produced by the parental plant (Ruyter and Stöckgit 1989; Schübel et al. 1989; Zhao and Verpoorte 2007).

The disadvantage for the commercial use of cell cultures is that most of them fail to produce the compound of interest, maybe for lack of precursors, or for the activity of the key enzyme in the metabolic pathway.

4.4.7 Biotransformation

Plant cells can use its biosynthetic machinery to catalyze the biotransformation of diverse compounds like phenolics, steroids, alkaloids, etc., by a wide variety of reactions (oxidation, reduction, hydroxylation, methylation, glycosylations, esterifications, etc.). They can act as biocatalysts of foreign and even synthetic molecules if the necessary enzymes are expressed in the plant cell (Giri et al. 2001). In general, the rate of conversion substrate-product is high and the reactions are stereo- and regiospecific, being the production costs justified by the added value of the product.

Considerable improvements have been done by genetic engineering, cloning in plant cells a foreign gene to induce or improve the biosynthesis of a specific compound. Conversely, genes codifying for plant enzymes have been cloned into microorganism to profit from their high productive rates (Alvarez and Marconi 2011).

4.4.8 Immobilization

Immobilization force plant cells to growth in close contact, in a microenvironment that brings the conditions to develop a certain degree of organization favourable to the production of the secondary metabolite. Basically, plant cells are entrapped in a polymeric matrix (alginate, agar, carragenanes, chitosan, gelatine beads or surfaces), and cultured in vessels in environmental conditions to maintain cells in the stationary phase of growth with a certain degree of structural and biochemical differentiation. The product is secreted into the culture medium and removed through classical downstream processing. The process can be developed in a semi-continuous or continuous operation.

Immobilization can also be combined with biotransformation or/and with elicitation. As an example, cell suspensions of *Vitis vinifera* and *Cruciata glabra* were immobilized in pectine/chitosan coacervate capsules and treated with chitosan or pectins as elicitors. The treatment produced an increase in the levels of hydrogen peroxide in both cases, and of anthocyanines in *V. vinifera* and anthraquinones in *C. glabra*. The same positive effect was of lower intensity in cells growing freely suspended, demonstrating the synergistic effect of immobilization and elicitation (Dörnenburg 2004).

4.5 Plant Transformation – Agrobacterium

In the 1980s the mechanism by which the natural plant pathogen *Agrobacterium* produces the crown gall disease in plants was elucidated. It was established that when *Agrobacterium* enters into the plant cell after a wound, introduces a fragment

of its plasmidic DNA (plasmid Ti or plasmid Ri in *A. tumefaciens* and *A. rhizogenes* respectively), which is integrated into the plant genome. The T region contains oncogenes that codify for enzymes that participate in auxin and cytokinin synthesis when expressed in plants. In the Ri plasmid, the genes codify for enzymes that determine high tissue sensitivity to PGR. The transformation with *A. rhizogenes* triggers the development of apical roots that will originate transformed roots, in the infection sites hairy roots. The transformation with certain strains of *A. tumefaciens* originates shooty teratomes. Once the transformed organ was obtained it can growth without any external supply of PGR.

The T-DNA also contains genes that codify for the synthesis of opines, used by bacteria as unique carbon and nitrogen sources, which are the base of the classification of the *Agrobacterium* strains (de la Riva et al. 1998).

4.5.1 Transformed Organs

Transformed roots obtained by infection with *A. rhizogenes* spp. (e.g.: LBA9402) are also called hairy roots for their abundant absorbent hairs. Shooty teratomes are obtained after transformation with *A. tumefaciens* strains (e.g.; T37) that contain genes for the synthesis of auxins (*aux1* and *aux2*) and cytokinins (*ipt*) that produced a reduced index auxin: cytokinin and as a consequence induces the production of stems.

Hairy roots have certain advantages respect to cell suspension cultures, they grow relatively faster, are biochemical and genetically stable, and produce a spectrum of secondary metabolites that quali- and quantitatively resembles those of the parental plants and in some cases are even more productive (Agostini et al. 2013; Ono and Tian 2011; Dörnenburg and Knorr 1995). Hairy roots allow the study of secondary metabolic pathways being relevant for the functional analysis of genes, plant physiology and metabolic research (Sharma et al. 2013; Hu and Du 2006). Also, they reunite the advantage of *in vitro* cultures with the presence of the *rol* genes that induce secondary metabolite pathways, even of those that are synthesized in aerial organs (Wheathers et al. 2005).

The genetic and biochemical stability of hairy root avoids the constant screening and selection of productive lines characteristic of undifferentiated *in vitro* cultures. The increased accumulation of certain secondary metabolites in hairy roots can be attributed to the fact that the *rolB* and *rolC* genes not only activate phytoalexin production but also suppress intracellular reactive oxygen species (ROS) levels (Bulgakov et al. 2011). Apparently, ROS mediate the elicitor-induced accumulation of isoflavonoids in species as *C. roseus*, *P. ginseng*, etc. (Zhao et al. 2005). The stimulator effect of *rolC* on growth and secondary metabolite production can be favorable in a production process. On the other hand, *rolB* that also has a positive effect on secondary metabolism is not attractive due to its inhibitor effect on growth (Bulgakov 2008).

Plant species	Compound	Reference	
Arachis hypogea	Stilbenes	Medina Bolívar et al. (2007)	
Artemisia dubia	Artemisinin	Mannan et al. (2008)	
A. indica			
A. lapathifolia	Peroxidases	Pérez et al. (2001)	
Scopolia parviflora	Scopolamine	Jung et al. (2003)	
Medicago trunculata	Carotenoids	Floss et al. (2008)	
Taxus cuspidata	Paclitaxel	Kim et al. (2009)	
Glycyrrhiza glabra	Fkavonoids	Li et al. (1998)	
Astragalus membranaceus Bge	Cycloartane	Ionkova et al. (2010)	
	Saponins		
D. straminium	Hyosciamine	Pavlov et al. (2009)	
Arachis hypogaea	Resveratrol	Condori et al. (2010)	
	Stilbenoids		
C. roseus	Ajmalicine	Wong et al. (2004)	
P. ginseng	Ginsenoside	Yu et al. (2005)	

Table 4.4 Compounds of plant origin produced in hairy root cultures

The different strategies applied to undifferentiated cultures in order to improve secondary metabolism production (culture medium composition, elicitators, precursors, etc.) were adapted to hairy root cultures (Elwekeel et al. 2012; Georgiev et al. 2012; Thimmaraju et al. 2003) (Table 4.4).

The production of tropane alkaloids by hairy roots of *Datura stramonium*, *Hyosciamus muticus*, *Brugmancia candida*, *Atropa belladonna* is an interesting example of the employment of different strategies. Elicitation, overexpression of key enzymes, genetic transformation with homologous genes, and the use as biocatalyzers of engineered *N. tabacum* and yeast overexpressing the *h6h* DNA gene were performed with different degree of success (Alvarez and Marconi 2011).

Even though the system has its advantages, their commercial application is not widespread. The main drawback for their massive culture is the characteristics of growth of the highly branched roots. Several attempts have been done to overcome that hurdle with a relative success (Medina-Bolivar and Cramer 2004).

An interesting development related to hairy root cultures is the Semiautomatic Image Processing System, RHYZOSCAN, a nondestructive analytical method, for determination of root architecture and secondary metabolite concentrations from scanned images (Berzin et al. 2000). The software resulted suitable for pigments or stainable products, because colour image analysis is implicated, but not appropriate for thick root clusters.

Hairy roots were not only used for producing plant metabolites but also for producing recombinant proteins. Chapter 5 summarizes some of advances in that field.

Also, a compilation of patents related to the application of hairy roots with different purposes (natural product production, bioremediation, etc.) can be find in Talano et al. (2012).

4.6 Metabolic Engineering

Metabolic engineering, synthetic engineering, and system biology engineering are devoted to elucidate biosynthetic pathways and also to offer the tools needed to improve yields (Mora-Pale et al. 2013; Wilson and Roberts 2014). Nevertheless, the number of commercial *in vitro* plant cell cultures processes for producing natural products remains low.

The accumulation and storage of secondary metabolites is the consequence of complex interactions among biosynthesis, transport, storage and degradation of the metabolite. Those processes are genetically regulated and the expression of the involved genes can be modulated through bioengineering, e.g.: by over-expressing the genes for key enzymes in the metabolic pathway (Verpoorte and Memelick 2002). An example of the successful implementation of metabolic engineering is the manipulation of anthocyanins and condensed tannin metabolism by regulating a family of transcription factors (MYB). The astringency, bitterness and color of fruits, the defence against predators (fungus and herbivores), and the forage quality can be manipulated in order to generate plants with the commercial desirable traits (Dixon et al. 2013).

Multiple-gene transformation of hairy roots has also been used to overexpress or suppress genes (Peebles et al. 2011; Huang et al. 2013b). An example is the culture of transgenic *C. roseus* hairy roots; the approaches employed were two *A, rhizogenes* strains carrying each one a binary vector with the marker genes, an *A. rhizogenes* with the transgenes in the same or different T-DNA region of a single binary vector. With the last two strategies, similar co-transformation efficiency was obtained despite of the high size of the vector plus transgenes. While, when the transgenes are in different binary vectors, the co-transformation efficiency was lower, perhaps for plasmid incompatibility. However, it can be an alternative tool when trying to introduce a large number of transgene in the plant genome (Huang et al. 2013b).

An example of the application of metabolic flux characterization is the production of geraniol engineered in tobacco hairy roots through the expression of geraniol synthase from *Valeriana officinalis* with/without geranyl phosphatase synthase from *Arabidopsis thaliana*, both plastid-targeted (Masakapalli et al. 2014). The effect of over-expressing geraniol synthase resulted in an increase of geraniol, as glycoside, effect that was not improved by the combined expression of enzymes. The major fluxes of central carbon metabolism did not show differences in the transgenic lines, and were not limited by substrate supply.

4.7 Recombinant Proteins

The expression of recombinant proteins in plants is also called molecular farming. The ability of plant to express foreign proteins was demonstrated at the end of the 1980s by several groups. In Belgium, the group headed by Schell and van Montagu

(Herrera-Estrella et al. 1983) described the use of *Agrobacterium* strains as a vector for introducing heterologous genes into plants. Since then, a huge number of proteins (enzymes, antibodies, antigens, etc.) were expressed in different plant species. Chapter 6 is devoted to this subject.

4.8 Scale-Up

The necessity of scaling-up the cultures of transformed organs triggered the development of bioreactors adapted to growing organs in liquid medium. After optimizing the productive process in Erlenmeyer flasks and analyzing the feasibility of a commercial exploitation, the next step is to scaling-up to bioreactors (Lee et al. 2004). Plant cells in culture have different characteristics than mammal and microbial cells (Table 4.5), as a consequence, there are some critical points to considered in order to adapt classical bioreactors to plant cell cultures.

4.8.1 Aeration

Oxygen requirement by plant cells is relatively low but can significantly increase during metabolite synthesis. The oxygenation is the main preoccupation of bioreactor design and scaling up since it limits cell growth, and consequently the volumetric productivity of high density and high viscosity cell suspensions. The adequate oxygen demand has to be established maintaining the adequate levels of CO₂ and other essential volatile compounds. The oxygen transference coefficient (Kla) has to be established (Thanh et al. 2006; Lee et al. 2011).

	o or microom, mainin	an, and plant con curtares	
Characteristics	Microbial cells	Mammal cells	Plant cells
Size	1–5 μ	10 ⁵ –10 ⁶ μ	10 ⁵ –10 ⁶ μ
Shear stress sensitivity	Low	High	High
Type of growth	Single cells	Single cells or surface adhered	Cell aggregates
Duplication time	<1 h	20 h	>24 h
Aeration	1–2 vvm	0.2 vvm	0.2 vvm
Nutritive requirements	Simple	Complex	Complex
Cell density	1010cells ml-1	106cells ml-1	106cells ml ⁻¹
Oxygen requirement	<180 mmol l ⁻¹ h ⁻¹	0.7-1.0 mmol l ⁻¹ h ⁻¹	0.5-1.8 mmol 1 ⁻¹ h ⁻

Table 4.5 Characteristics of microbial, mammal, and plant cell cultures

4.8 Scale-Up 49

4.8.2 *Mixing*

It is essential to have a homogenous distribution of cells, nutrients and products. Mixing is performed with aerators, mechanical stirrers or a combination of both. The magnitudes of hydrodynamic forces associated to mixing must be sufficiently low as to not cause cell death and to stimulate certain cell functions.

In mechanically agitated bioreactors, different types of impellers are used to agitate medium (flat-blade turbine impeller, helical ribbon impeller, vibrating perforated plates). Pneumatically agitated bioreactors can be bubble columns where air is bubbled at the base of the column, or air lift where air is sparged from the riser section to the top of the column and then the medium descends in the down corner section.

4.8.3 Culture Medium Selection

The selection of the operation condition (batch, fed-batch or continuous culture) depends on the dynamic of the specific culture. Batch cultures are characterized by conditions constantly changing, metabolites are produced associated to a kinetic pattern, and the culture medium is, generally, the one optimized at lab scale.

Fed-batch cultures are those with t a controlled addition of nutrients, generally a limiting one that permits the study of the conditions for maximal productivity in long periods of time.

Continuous culture maintains cells in stationary state (chemostat) with a constant supply of culture medium and cells; it is usually designed for producing a high volume of low value products associated to growth, typically primary metabolites and biomass (Bondarev et al. 2003; Antoniukas et al. 2006; Desai et al. 2006).

4.8.4 Bioreactors

In a bioreactor, the optimization implies a balance between biological and engineering factors to obtain high productivity at minimal costs. Plants cells are characterized by slower growth, lesser oxygen demand, and higher sensibility to shear stress than microbial cells, and also by the tendency to form clusters by aggregation. Thus, the culture of plant cells in bioreactors requires of specific aeration and mixing devices.

The design of the bioreactor is a key factor for providing an accurate mixing and mass transfer minimizing the intensity of shear stress and hydrodynamic pressure. Thus, the design of bioreactors involves taking into account all that characteristics of plant cells (particularly shear stress, doubling time, photoperiod, etc.).

The type of bioreactor (stirred, air lift, plastic sleeve) (Table 4.6) must be selected considering the type of operation to be conducted (batch, fed-batch, continuous),

Bioreactor	Advantages	Disadvantages
Stirred tanks	Flexible, high coefficient of mass transfer, homogenous, useful for high density cultures, useful for working with GMPs.	Shear stress, expensive, risks of contamination (valves), heat emission.
Pneumatics (bubble column) bioreactors	Easy scale-up, low costs, low contamination risks, low shear stress, low heat emission.	Low oxygen transfer, inefficient mixing in high viscosity cultures, foam production at high aeration.
Pneumatics (airlift)	Bubbling driving, good oxygen transfer, low shear stress, without heat emission, low mixing times, low costs, easy scale-up, efficient fluid circulation.	Inefficient mixing in high viscosity cultures, foam production at high aeration.
Wave reactor	Without shear stress, good oxygen transference, low operational costs.	Scale-up, heat emission.
Membrane-reactor	Removal of extracellular products, low shear stress, low operational costs.	Scale-up, oxygenation, low heat transference, on-line monitoring.

Table 4.6 Advantages and disadvantages of bioreactors for plant cultures

and the behavior of the metabolite to be produced (secreted or not to the culture media, produced associated or not to growth, etc.).

Strategies as elicitation, removal of products *in situ* to avoid feedback inhibition, etc., are also valid.

Other parameters to be optimized are the simplicity and celerity of the biomass harvest and of product extraction, purification and quantification (Archambault et al. 1996; Chaterjee et al. 1997; James et al. 2002; Komar et al. 2004; Dewir et al. 2006; Curtis 2005; Huang and Mcdonald 2009; Donnez et al. 2011; Ferri et al. 2011; Baque et al. 2012).

Batch culture is a close system where the inoculum is fixed at the beginning of the process. The conditions in the vessel change as the nutrients are consumed and end products accumulate. In general the kinetic of growth is a sigmoid curve with a lag, exponential and stationary phase, the last when the culture enters in senescence.

Fed batch culture receives periodically fresh culture medium to maintain plant biomass growth (in a linear relationship).

Continuous culture receives fresh medium during the exponential phase of growth and a similar volume of culture is retired in order to maintain the volume in the vessel.

During the whole process the fundamental parameters of culture must be monitored. Some parameters are monitored on-line (temperature, pH, dissolved oxygen, carbon dioxide, foam) while others are off-line controlled (cell concentration and viability, tissue morphology, substrate and product concentration) (Forcato et al. 2002; Nadadoor et al. 2012).

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4.9 Modeling

Mathematical models are essential for understanding the behavior of cultures under different conditions. Chapter 9 is dedicated to the subject of mathematical modeling in *in vitro* cultures.

4.10 Conclusive Remarks

Only a few productive processes for producing secondary metabolites using *in vitro* cultures were commercially established, although there is a great amount of knowledge generated about biosynthetic pathways, methods for optimizing yields, large-scale operations, etc.

Up to now, large-scale processes have only been developed in a few countries (Japan, Russia. Germany). Japan has promoted this technology with strong politics of academy-industry collaboration. As a result the dye shikonine is produced by *in vitro* cultures of *L. erythrorizon* in a commercial scale (Japan Tobacco Inc's). Japan also produces alkaloids, steroids, etc. in *in vitro* cultures of *Panax ginseng* (Meiji Seiko, Ajinomoto and Nippon Shin-Jaki) (Yesil Celiktas et al. 2010; Curtin 1983).

The limited industrial applications of *in vitro* cultures for producing secondary metabolites in other countries are mainly attributed to the low yields and the loss of the productive capability with time of those cultures. Optimization through bioreactor design can be of great help for large-scale production.

New devices, (e.g. meshes to growth hairy roots), or the induction of a certain degree of organization in single cell cultures (e.g.: immobilization) can generate the conditions that cultures need to reach their maximal biosynthetic capacity.

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Chapter 5 Solasodine Production in Solanum eleagnifolium in vitro Cultures

Abstract *Solanum eleagnifolium* Cav. var leprosum (Ortega) Dunal is a species that grow in Argentina. It is characterized for accumulating, mainly in green fruits, the glycoalkaloid solasodine, the nitrogenated analogue of diosgenine, which can be used for the synthesis of steroidal compounds (e.g.: contraceptives and corticosteroids).

In vitro cultures of S. eleagnifolium Cav. were established, and the conditions for achieving high solasodine yields were studied. Plant growth regulators balance, the age and size of the inocula, the conduction of the productive process in undifferentiated cultures and in hairy roots and transformed stem cultures were studied. Also, an approach to large-scale culture was performed. Plant growth balance appeared as the most significant strategy for improving solasodine yields in undifferentiated in vitro cultures of S. eleagnifolium Cav.

On the other hand, the solasodine levels attained in hairy root cultures were the highest, demonstrating that differentiation is related to the amount of for solasodine produced.

Keywords *Solanum eleagnifolium* Cav • Solasodine • *In vitro* cultures • Solasodine productivity • *Agrobacterium rhizogenes*

5.1 Introduction

Steroidal glycoalkaloids are a chemical group with particular biological activities that range from antimicrobial to analgesia, among others (Patel et al. 2013) (Table 5.1).

A representative of the group is solamargine (Fig. 5.1, II), a steroidal glycoalkaloid that can be used for the synthesis of steroidal compounds of pharmaceutical interest, such as steroidal contraceptives and corticosteroids (Mann 1978). Formerly, those compounds were produced exclusively from diosgenine, a steroidal glycoalkaloid present in the Dioscoreacea family. Their irrational exploitation caused a shortage of raw material with an increase of production costs promoting the search of alternative sources. Solasodine (Fig. 5.1, I) is the nitrogenated analogue of diosgenine, that can be used for the synthesis of 16-dehidropregnenolone and different steroidal hormones by chemical or microbial transformation (Rodriguez 1984). It is found in

Activity	Species	Active molecule/s	Reference
Analgesic	S. xanthocarpum	Solasodine	Gangwar et al. (2013)
Bronchodialator		Solasodine sapogenin	Kajaria et al. (2012)
Antiandrogenic			Khatodia et al. (2013)
Angiotensive	S. laciniatum	Solasodine	Shakirov et al. (2012)
Antineoplasic		Solasodine	Cham (2014)
		Rhamnosides	Cham (2008)
		Solamargine	
		Solasonine	
Anti-asmathic	S. khasianum	Solamargine	Tambe (2013)
Contraceptive		Solasonine	
Anticancerigen			

 Table 5.1
 Some biological activities of steroidal glycoalkaloids found in species of the Solanum genus

Fig. 5.1 Chemical structures of Solasonine (I), Solamargine (II) and Solasodine (III)

relatively high concentrations in leaves and fruits of a variety of species from the genus Solanum, as *S. laciniatum*, *S. aviculare*, *S. khasianum*, *S. marginatum*, and *S. eleagnifolium* (Rodríguez et al. 1979; Mann 1978; Guerreiro et al. 1971; Telek et al. 1977; Schreiber 1963; Schreuber 1968) (Table 5.2).

Species	Plant organ	Glycoalkaloid content (g kg ⁻¹ DW)	Glycoalkaloid
S. eleagnifolium Cav. var. leprosum	Green fruits	70–72	Solamargine
S. lorentzii Bit	Leaves and branches	10–37 Solam	
S. calophyllum Phil	Leaves and branches	5.76	Solasodine
S. juncallense Reiche	Leaves and branches	5.05	Solamargine
S. sublobatum Willd	Fruits	11.60	Solamargine
S. atriplicifolium Gill	Fruits	_	_
S. euacanthum Phil	Leaves and branches	3.5	Solamargine
S. pyrethifolium Griseb	Leaves and branches	12.5	Solamargine
S. juvenale Thell	Leaves and branches	_	-

Table 5.2 Glycoalkaloid content of *Solanum* species from Argentina

5.2 Solanum eleagnifolim Cav.

From the *Solanum* species that grow in Argentina, *S. eleagnifolium* Cav. var leprosum (Ortega) Dunal ("meloncillo del campo", "quillo", "revienta caballo") is the one with the highest solamargine content (Guerreiro et al. 1971). It is a perennial plant, 30–50 cm of height, with a branched stem covered by stellate trichomes and yellow stings. Leaves are numerous, alternated, covered by hairs and thorns along the petiole and nerves, both in the upper and lower surfaces. The radical system is dimorphic, with a vertical strong root, with diageotropically growth, that originates lateral roots that can extend to a distance of approximately 3 m. Flowers are blue, and are placed both in axial and terminal position. Fruits are berries of 6–8 mm diameter, each one with 40–50 seeds agglutinated by a saponin-rich substance. It is considered a toxic species especially for horses and cattle.

Usually, *S. eleagnifolium* Cav. grow in warm-temperate fertile soils, however, it can also be found in sandy or saline semiarid soils. In Argentina, it is distributed in the Cuyo region and in the Pampa cultivated areas.

Plants reproduce by seeds that germinate from September to December, in a first germination period, and in a second term in February. The presence of steroidal glycoalkaloids (e.g.: solamargine, solasonine) was established in different organs of the plants, but the highest levels are found in green fruits (Rodriguez 1984). In the plant, solasodine is present as a glycoside, whose sugars are bonded to the C3-hydroxyl group.

Several glycosides were described; the most frequent are solasonine and solamargine (Fig. 5.1, II), the last the most abundant. The glycosides are extracted from

Method	Sensibility	Reference
Gravimetric	Milligrams	Bell and Briggs (1942)
Tritimetric	Milligrams	Bite et al. (1970), Hardman and Williams (1971), Weiler et al. (1976)
Colorimetric	10–100 μg	Saini et al. (2007), Lancaster and Mann (1975)
Chromatographic	Nanograms	Trivedi and Pundarikakshudu (2007), Magrini et al. (1989), Crabbe and Fryer (1982), Herb et al. (1975)
Radioimmunoassay	Nanograms	Weiler et al. (1980)

Table 5.3 Methods for quantifying solasodine glycosides

S. eleagnifolium Cav. fruits by chemical or microbiological hydrolysis (Rodriguez 1984; Weston 1976; Regerat and Pourrat 1981; Ehmke 1986).

Solasodine can be determined by different analytical methods each one with different sensibility (Table 5.3): (a) Gravimetric (Bell and Briggs 1942), (b) Tritimetric (Bite et al. 1970), which detect milligrams of product, are fairly unspecific, and require an extensive purification that reduces the precision of the assays (Hardman and Williams 1971; Weiler et al. 1976), (c) Colorimetric, which is based on the development of colour by chemical reactions with the quaternary nitrogen of the molecule. The absorbance is read in a UV-visible spectrophotometer at a wavelength of 425 nm. The range of detection is 10– $100~\mu g$ of solasodine (Saini et al. 2007; Lancaster and Mann 1975), (d) Chromatographic, as thin-layer chromatography (TLC), High Performance Thin Layer Chromatography (HPLC), and gas chromatography (GC) that are more sensitive than the formers (Trivedi and Pundarikakshudu 2007; Magrini et al. 1989; Crabbe and Fryer 1980; Herb et al. 1975), and (e) Radioimmunoassay which detects nanograms of solasodine glycosides (Weiler et al. 1980).

The production of solasodine was studied in plants growing in the field, focused on the analysis of the influence on yields of different factors such as influence of weather, nutrients, harvest method, processing of raw material, etc.

Nigra et al. (1990) have demonstrated the ability of *S. eleagnifolium* Cav. *in vitro* cultures to produce solasodine. The *in vitro* cultures are a recognized alternative production platform of secondary metabolites (Chap. 4). *In vitro* cultures have the advantage that it can be developed in controlled environmental conditions, free of pathogens, and with the possibility of a tight control of the phytofermentative process. With that background information, we have studied the *in vitro* establishment of *S. eleagnifolium* Cav. high producing lines through the selection and multiplication of solasodine-rich individuals or cultures. Also, we have studied the influence of plant growth regulators (PGR), and the establishment of transformed cultures (shoots and hairy roots) and their solasodine content.

The experimental scheme followed was: (a) Selection of producing and stable calli lines; (b) Study of the influence of PGR on the initiation and maintenance of clones and on cell growth and solasodine yield. These studies were performed both in calli as in cell suspension cultures; (c) Determination of the optimum inoculum size and age to initiate the phytofermentative process in suspension cultures; (d) Determination of the solasodine content in hairy roots and transformed stems obtained by transformation of *S. eleagnifolium* Cav. with *Agrobacterium* spp. (Fig. 5.2).

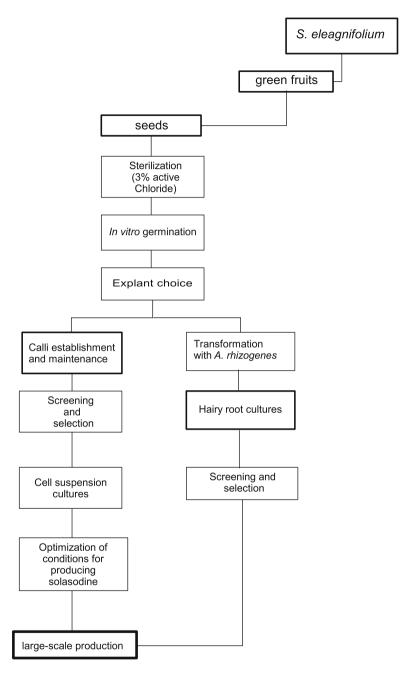


Fig. 5.2 General scheme of the procedure followed to analyze solasodine production by *S. eleagnifolium* Cav. *in vitro* cultures

5.3 Establishment of S. eleagnifolium Cav. in vitro Cultures

5.3.1 Establishment of Calli Culture

Calli were initiated according to Nigra et al. (1987). Briefly, seeds from green fruits collected in San Luis, Argentina, were washed and sterilized using NaClO (4 % active Cl2) and Tritón X-100 (0.1 %). Then, they were transferred to flasks containing MSRT culture medium (Nigra et al. 1987) with the addition of agar (8 g l⁻¹), and kept in growth chamber at 24 ± 2 °C and a 16-hs photoperiod given by fluorescent lamps (irradiance 1.8 w m⁻¹ seg⁻¹). After 3–4 weeks axenic plantlets developed from sterilized seeds (germination index: 40 %, contamination index: 5 %). Pieces of hypocotyls of approximately 1 cm length were transferred to flasks containing the same MSRT culture medium, with the addition of sucrose (30 g l⁻¹) and different auxins as PGR (Table 5.4). Flasks were maintained in a culture chamber at the same conditions described above.

Regions of hyperplasia appeared only in explants cultured in medium A after 8 days in culture. In the other media, morphological changes were only evident after 4 weeks in culture. After 8 weeks in culture, calli developed from explants in medium A, calli and thick roots grow in media B and C, the whole plant regenerated in medium D, and primordial non-proliferating buds developed in medium E.

Calli initiated in medium A were transferred to A, B, C, D, and E fresh media. The first weeks, calli proliferated in the four media but after 4 months calli turned necrotic in media C, D, and E, perhaps as a result of the disappearance of any residual 2,4-D content.

At the concentrations used, 2,4-D is the PGR of election for calli initiation, IBA does not induce calli, IAA induces the regeneration of the whole plant and NAA and 2,4,5-T resulted rhizogenic. Thus, IBA, IAA and NAA are not an adequate PGR for calli maintenance. Calli maintained in media A are green, friable, and sustains its growth rate (μ =0.08), doubling time (td=8.66 days), and growth index (15.5), and its viability and capability of producing solasodine for more than 2 years in *in vitro* conditions.

To evaluate solasodine content, samples are taken every 15 days (10 samples per each treatment), and maintained at 40 °C until constant weight. Solasodine was evaluated by the methods established by Lancaster and Mann (1975) and Magrini et al. (1989). The results were statistically analyzed by regression.

Solasodine content in calli varies according to the PGR used. Only 2,4-D and 2,4,5-T were able to maintain growth and solasodine production. In the case of 2,4,5-T, solasodine level is around an average value of 0.55±0.058 mg g DW⁻¹, which is similar to that reported in *S. laciniatum* Alt. In this case calli growing with 2,4-D (1–2 ppm) as PGR have a solasodine yield of 0.5 mg g DW⁻¹ (Hosoda et al. 1979). On the other hand, 2,4-D as PGR gave a highest solasodine initial amount (1.3 mg g DW⁻¹) during the first subcultures but the solasodine yield fell down in the subsequent subcultures (Fig. 5.3). In conclusion, 2,4,5-T allows constant relatively high solasodine amounts while 2,4-D allows highest solasodine amounts during the first months in culture but the productive capacity of the cultures decreases with time in culture (Nigra et al. 1989).

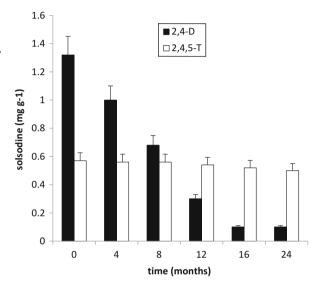
Calli lines were identified and selected according to their solasodine yield. They were classified in low producing lines (<1 mg solasodine g DW⁻¹), lines that initially

Table 5.4 Culture media used to establish *S. eleagnifolium* Cav. *in vitro* cultures

Medium	Basal medium	Auxins
A	MSRT	2,4-D (4.5 μM)
В	MSRT	2,4,5-T (3.91 μM)
С	MSRT	NAA (5.37 μM)
D	MSRT	IAA (5.70 μM)
Е	MSRT	IBA (4.90 μM)

2,4-D: 2,4- dichlorophenoxy acid; 2,4,5-T: 2,4,5-trichlorophenoxy acid; NAA: naphthalene acid; IAA: indole acetic acid; IBA: indole butyric acid

Fig. 5.3 Variation with time of solasodine content in S. eleagnifolium Cav. calli maintained in medium MSRT supplemented with 2,4-D (4.5 μM) or 2,4,5-T (3.91 μM) as PGR



showed high solasodine content (>4 mg solasodine g DW⁻¹) that fell down after several subcultures, and lines with a stable solasodine content (around 1.5 mg solasodine g DW⁻¹). From the lines developed, line 009 was selected for further experiments considering its high and stable solasodine yield.

5.3.2 Establishment of Cell Suspension Cultures

Friable calli from the selected line were transferred to 200 ml-Erlenmeyer flasks containing 40 ml MSRT culture medium without agar and with the addition of different PGR (Table 5.5). Cultures were incubated at 24 ± 2 °C, 16-h photoperiod (irradiance=1.8 w m⁻² s⁻¹) in rotary shaker at 120 rpm. The obtained cell suspensions were transferred to identical fresh culture medium each 15th day, samples were taken in each subculture to analyze the cells microscopically.

Cell suspensions initiated in media C and D were heterogeneous, with green-brownish clumps, that show free cells or in small aggregates under the optical microscope. In media A and B cell suspensions are homogeneous, showing tubular

Table 5.5 Culture media used to initiate cell suspension cultures of *S. eleagnifolium* Cav

Culture medium	Basal medium	Auxins
A	MSRT	2,4-D (4.5 μM)
В	MSRT	2,4,5-T (3.91 μM)
С	MSRT	NAA (5.37 μM)
D	MSRT	ΙΑΑ (5.70 μΜ)

free cells with thin walls under the optical microscope. The presence of aggregates in medium C and D do not allow a homogeneous transference of mass and energy as happen in homogeneous cell suspension cultures. Thus, cell suspension cultures in media A and B were selected for further experiments since the homogeneity of transference is a key factor for conducting a biotechnological process.

5.4 Influence of Plant Growth Regulators

In order to analyze the influence of PGR on cell growth and solasodine production, 7-days old suspended cells maintained in medium A were filtered through sterile plastic sieves (40 mm mesh diameter) to retain cell aggregates, and transferred to 40 ml Erlenmeyer flasks, at a 5 % V/V inoculum size, containing one of the media described in Table 5.6. Cultures were developed at the same conditions described above during 25 days, every 5 days 3 ml-samples were harvested to determine packed cell volume (PCV), dry weight (DW) and solasodine content. Growth Index and solasodine productivity are shown in Table 5.7.

Cell viability was determined combining the Evans blue method with a treatment with fluorescein diacetate (FDA). Viable cells do not embody the blue dye and are fluorescent under the UV-light. Viability index (VI) was determined by determining the percent relationship among live cells and dead cells (Alvarez 1992, PhD Thesis).

Figure 5.4 shows the cell growth and viability in cell suspension cultures growing in medium A. The growth curve shows no initial lag phase, an exponential phase with a constant growth up to the 10th day of culture, followed by a stationary phase that maintains up to the end of the culture with a final biomass of 4.2 mg DW ml $^{-1}$. Under the microscope cells are isodiametric in the early exponential phase, and then they elongate and bond by their minor walls in aggregates of no more than 4–6 cells. As for the viability index, it stays over 80 % during the first 25 days, being the optimal timing for transference between the 10th and 20th day (VI=98 % and 85 % respectively) (Fig. 5.4).

To analyze the effect of different relationships auxin: citoquinine on solasodine production, cell suspension cultures were transferred to MSRT medium with each one of the PGR relationship showed in Table 5.8. Cultures were developed during 25 days, 3 ml-samples were taken every 5 days to analytical studies.

After 10 days in culture, the highest GI and solasodine content were attained with low concentrations of kinetin (0.25, 0.50 and 1.0 μ M). The productivity reached in the presence of NAA (2.54±0.22 mg l⁻¹ day⁻¹) was significant higher (P<0.05) to those attained in the presence of 2,4-D (0.50 mg l⁻¹ day⁻¹) (Table 5.9). The growth curves

Culture medium	Basal medium	Auxins (μN	(I)
A1	MSRT	2,4-D	0.5
A2	MSRT		5
A3	MSRT		50
B1	MSRT	NAA	0.5
B2	MSRT		5
В3	MSRT		50
C1	MSRT	IAA	0.5
C2	MSRT		5
C3	MSRT		50
D1	MSRT	2,4,5-T	0.5
D2	MSRT		5
D3	MSRT		50

Table 5.6 Culture media used to analyze the influence of PGR on cell growth and solasodine content in *S. eleagnifolium* Cav. cell cultures

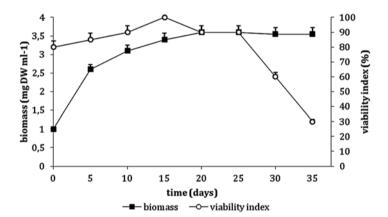


Fig. 5.4 Cell growth (mg DW biomass ml $^{-1}$) and viability index (%) of S. eleagnifolium Cav. cell suspension cultures in MSRT media with 2,4-D 4.5 μ M

show that the higher productivity corresponds to the 10th day of culture and immediately sharp fall down, probably due to a solasodine degradation process (Fig. 5.4).

In suspension cell cultures growing in MSRT media with 2,4-D as PGR the specific growth rate is high (μ =0.34 days⁻¹) but the solasodine productivity is poor (0.58±0.15 mg l⁻¹ day⁻¹) while in the presence of NAA (50 μ M) and kinetin (0.25 μ M) as PGR, cells grow slowly (μ =0.14 days⁻¹) but solasodine productivity and yield are higher (2.54±0.22 mg l⁻¹ day⁻¹ and 6.98 mg g⁻¹ respectively) (Fig. 5.5). The production of solasodine resulted strongly influenced by the PGR relationship; it is inhibited by a high 2,4-D concentration and by the PGR 2,4,5-T and IAA. From the auxins tested, NAA seems to be the most effective promoting solasodine production particularly in the presence of kinetin (0.25 μ M) (Alvarez et al. 1993). These results are in according to those obtained for the production of anthraquinone by *Morinda citrifolia* and *Rubia cordifolia* (Zenk et al. 1975; Suzuki et al. 1987),

Table 5.7 Variation of growth index (GI) and productivity (mg gDW⁻¹ l⁻¹) os *S. eleagnifolium* cell suspension cultures after 10 days in culture in the different media tested

Auxin (µM)	1	Growth index (%)	Solasodine productivity (mg l ⁻¹ day ⁻¹)
2,4-D	0.5	14	0.60
	5	13	0.60
	50	12	0.50
2,4,5-T	0.5	1	0.05
	5	0.8	0.20
	50	0.2	0.28
IAA	0.5	3	0.22
	5	5	0.40
	50	3	0.30
NAA	0.5	19	0.30
	5	15	0.48
	50	19	0.80

ANOVA analysis was performed in all the experiments. From all the PGR tested, 2,4-D and NAA have a positive effect both on cell growth and solasodine production

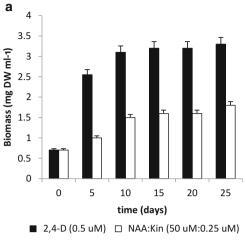
Table 5.8 Different hormone relationships used to evaluate solasodine productivity of *S. eleagnifolium* Cav. cell suspension cultures

Kinetin (µM)	2,4-D (µM)	2,4,5-T (µM)	NAA (μM)	IAA (μM)
0	0.5	0.5	0.5	0.5
	5	5	5	5
	50	50	50	50
0.25	0.5	0.5	0.5	0.5
	5	5	5	5
	50	50	50	50
0.5	0.5	0.5	0.5	0.5
	5	5	5	5
	50	50	50	50
5.0	0.5	0.5	0.5	0.5
	5	5	5	5
	50	50	50	50
10	0.5	0.5	0.5	0.5
	5	5	5	5
	50	50	50	50

Table 5.9 Influence of kinetin on growth index (GI) and productivity of *S. eleagnifolium* Cav. cell suspension cultures

$Kinetin \left(\mu M \right)$	(μM) Auxin (μM)		Growth index (%)	Solasodine productivity (mg l ⁻¹ day ⁻¹)	
0 (control)	2.4-D	0.5	14.8	0.58	
0.25		0.5	2.0	1.0	
0.5		0.5	1.9	1.3	
1.0		0.5	2.8	1.4	
0.25	NAA	50	4.0	2.5	
0.5		50	0.6	1.9	
1.0		50	0.4	1.8	

C: control MSRT medium with 2,4-D (0.5 μ M). Culture period: 10 days



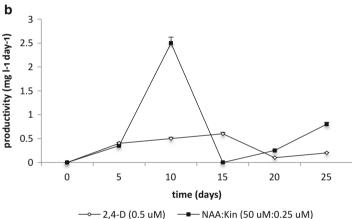


Fig. 5.5 (a) Cell growth and (b) solasodine productivity (at the 10th day of culture) in cell suspension cultures of *S. eleagnifolium* growing in MSRT+2,4-D (0.5 μ M) or MSRT+NAA (50 μ M): kinetin (0.25 μ M)

rosmarinic acid by *A. officinalis* (De-Eknamul and Ellis 1985), and berberine by *T. minus* (Nakagawa et al. 1986).

The experiments also show that the PGR relationship for optimal growth is different from those for optimal solasodine production, which suggest that a two-step productive process could be successful, as it was for the production of berberine by *Berberis buxifolia* Lam. (Alvarez et al. 2009). In such a dual system S. *eleagnifolium* Cav. cells could proliferate in MSRT medium with 0.5 μ M 2,4 D as PGR and then they could be transferred to a productive medium with NAA (50 μ M) and Kinetin (0.25 μ M) as PGR.

The combination of other citoquinines (BAP and zeatin) with auxins (2,4-D $0.5~\mu M$ and NAA $50~\mu M$) was tested for studying their effect on solasodine production (Table 5.10). Cell growth increased at all the combinations tested, which is in agreement with the fact that the external supply of citoquinines (especially of a

Citoquinine (µM)		Auxin (μΝ	Auxin (μM)		Solasodine yield (mg g ⁻¹)
Zeatin	0	NAA	50	12.5	3.2
	0.25			40.5	0.8
	0.50			31.0	3.8
	1.0			31.0	1.2
BAP	0.25		50	25	2.9
	0.50			29	1.0
	1.0			11	2.0
Zeatin	0.25	2,4-D	0.50	30	5.0
	0.50			39	1.1
	1.0			40	2.0
BAP	0.25		0.50	15	4.8
	0.50			17	6
	1.0			15	2.8

Table 5.10 Influence of zeatin (Z) and 6-benzyl aminopurine (BAP) on growth index (GI) and solasodine yield in *S. eleagnifolium* Cav. cell suspension cultures

C: control medium (MSRT medium + 2,4-D 0.5 µM). Culture period: 20 days

natural citoquinine as zeatin) induces cell division (Nishinari and Syono 1980). As for solasodine yield, with the relationship 2,4-D (0.5 μ M): BAP (0.5 μ M) a value of 6.00±0.04 mg g⁻¹ was attained that is comparable to those obtained with NAA (50 μ M): kinetin (0.25 μ M). For all the PGR relationship tested, solasodine was not detected in the culture medium.

As a conclusion, from the assays performed for determining the influence of PGR on solasodine production by *S. eleagnifolium* Cav. the best amounts were obtained with NAA: Kinetin (0.5 μ M:0.25 μ M) and 2,4-D: BAP (0.5 μ M:0.5 μ M) which are comparable to those measured in the wild plant (Guerreiro et al. 1971).

5.5 Influence of Inoculum Age and Size

For inoculum size experiments, 21-days-old cell suspension maintained in MSRT medium with 2,4-D (5 μ M) were washed five times with MSRT medium without PGR and then transferred to 200 ml-Erlenmyer flasks containing 40 ml MSRT medium with NAA: kinetin (50 μ M: 0.25 μ M) as PGR. The inoculum sizes tested were 5 %, 10 % and 20 % v/v.

For inoculum age experiments, 3, 8, 15, and 19-days-old-cell suspension cultures at a 5 % inoculum size were inoculated in 200 ml Erlenmyer flasks containing 40 ml MSRT culture medium with 2,4-D: kinetin (5 μ M: 0.25 μ M) as PGR. Cultures were maintained during 25 days at 24±2 °C, 16-h photoperiod in a rotary shaker at 120 rpm. Samples of 3 ml were taken each 5 days for determining biomass and solasodine content.

From the inoculum sizes tested, the highest biomass (3.6 mg g DW⁻¹) was attained at a 20 % v/v inoculum size (P<0.10) and the highest solasodine yield with an inoculum size of 5 % (4.0±0.35 mg g DW⁻¹). Fujita et al. (1985) working with *L. erythrorhizon* for producing shikonine also observed that converse relationship between yields and inoculum size. As for the inoculum age, a 19-days old inoculum produces the highest solasodine yields (2.7±1.51 mg g DW⁻¹) but no significant differences were observed in biomass yield (P<0.05) (Parsons et al. 2001).

5.6 Transformed Stems and Hairy Roots

Previous studies (Nigra et al. 1989) had demonstrated that solasodine yields increased in the presence of certain degree of differentiation induced by PGR relationship.

On the other hand, Lancaster and Mann (1975) reported that for *S. laciniatum* Ait, the solasodine concentration in the wild plant reached their highest value in green fruits but that during fruit maturation the alkaloid disappeared. Czygan and Willuhn (1967) suggested that the alkaloid metabolites could be involved in carotenoid biosynthesis in the mature fruits. Also, Lancaster and Mann (1975) demonstrated that the decrease in the total solasodine amounts were accompanied by an increase in the total amount in roots, suggesting that solasodine cold be transported from the mature organs to the roots to accumulate there. That phenomenon of translocation of metabolites is a quite general phenomenon described in several species. Based on those observations, the analysis of solasodine production in transformed organs was performed considering their characteristics of higher genetic and productive stability.

5.6.1 Hairy Root Cultures

A. rhizogenes LBA strains 9402 and 9816 were maintained in YMB medium. Stems and leaves of *S. eleagnifolium* Cav. axenic plantlets were infected with 48-h A. rhizogenes cultures cultured at 28 °C, with the addition of acetosyringone (0.1 % P/V). Infected explants were transferred to MSRT solid medium without the addition of PGR and cultured at 24±2 °C and 16-h photoperiod. After 2–3 weeks root apex that appeared in the infection sites, were excised and transferred to MSRT culture medium in the presence of ampicillin 0.2 % to eliminate *Agrobacterium*.

When the cultures showed absence of *Agrobacterium*, the roots were transferred to MSRT medium without the addition of PGR and antibiotics. Transformation was confirmed by PCR using primers for *rolB* to amplify a 700 bp fragment as was described by Hamill et al. (1989). The transformation efficiency was 80 %.

Several clones were obtained, with different morphological characteristics and fast growth. The clones 1 and 2 were 2 the best productive with solasodine yields of 1.9 ± 0.3 mg g⁻¹ and 1.175 ± 0.3 mg g⁻¹ respectively.

5.6.1.1 Kinetic of Growth and Production of Solasodine of S. eleagnifolium Cav. Hairy Roots

Clone 1 was used for performing these experiments for their characteristics of growth and solasodine production. Apexes of hairy roots (3.5 mg \pm 0.5 mg DW) were transferred to 250 ml Erlenmeyer flasks containing 40 ml MSRT medium without PGR. Cultures were performed at 24 \pm 2 °C, 16-h photoperiod, 1.8 w m⁻² s⁻¹ irradiance and 100 rpm during 30 days. Samples of 3 Erlenmeyers were taken each 5 days to evaluate growth and solasodine content.

The kinetic of growth and solasodine production is shown in Fig. 5.6. In hairy roots a lag phase is followed by an exponential phase of 10 days before entering in

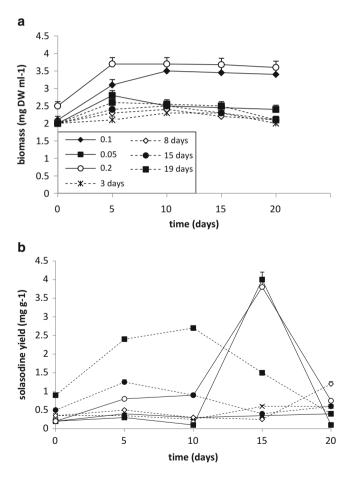


Fig. 5.6 Influence of inoculum size and age on biomass (a) and solasodine (b) yields by *S. eleagnifolium* Cav. cell suspension cultures in MSRT culture medium with NAA (50 μ M): Kinetin (0.25 μ M) as PGR

Table 5.11 Comparison of the specific growth rate, growth index, doubling time, final biomass, and solasodine yield of hairy roots and calli growing in MSRT medium with 2,4-D (4.5 μ M) and 2,4,5-T (3.91 μ M)

Parameter	Hairy roots	Calli MSRT+2,4-D (4.5 μM)	Calli MSRT+2,4,5-T (3.91 µM)	Cell suspension cultures MSRT+NAA: kin (50 µM: 0.25 µM)	Cell suspension cultures MSRT+2,4-D: BAP (0.5 µM: 0.5 µM)
μ (days)	0.55	0.08	0.08	0.14	0.54
td	30 h	8.66 days	8.45 days	4.95	2.03
Final biomass (mg FW ⁻¹)	140	180	104	83	102
GI	39	45	41	4	17
Solasodine yield (mg g ⁻¹)	1.90±0.08	1.3±0.08	0.55 ± 0.09	6.98±0.5	6.00 ± 0.5

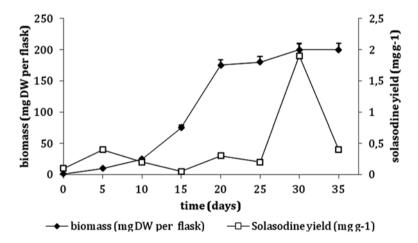


Fig. 5.7 Kinetic of growth and solasodine yield of S. eleagnifolium Cav. hairy root, clone 1

stationary state (Alvarez et al. 1994). A comparison among the specific rate of growth, growth index, doubling time, final biomass and solasodine yield of hairy roots and calli rowing gin MSRT medium with 2,4-D (4.5 μ M) and 2,4,5-T (3.91 \pm M) are shown in Table 5.11 (Fig. 5.7).

5.6.2 Transformed Stems

Plantlets were transformed using 48 h old-culture of *A. tumefaciens* strain T37 maintained in trypton-yeast culture medium (Ty) at 28 °C. Infected plantlets were transferred to solid MSRT culture medium at 24 ± 2 °C, 16 h photoperiod. When the buds appeared at the infection points, they are transferred to MSRT liquid medium containing ampicillin (0.5 %) to eliminate the bacteria. Transformation was confirmed according to Otten and Schilperoot (1978). The efficiency of transformation was 76 %. Several clones were obtained; the independence of the exogenous supply of PGR is evident, as was also determined by Spencer et al. 1990; Gresshoff et al. 1979; Ooms et al. 1981. We selected those that produced significant amounts of solasodine. In average, the growth index was 54.4 and the solasodine yield was 0.35 ± 0.09 mg g⁻¹ which is comparable to the values obtained in stems and leaves of the wild plant and was lower to those values in the best performing undifferentiated *in vitro* cultures.

5.7 Conclusive Remarks

Different strategies were used to analyze solasodine production by *S. eleagnifolium* Cav. *in vitro* cultures. Plant growth balance appeared as the most significant strategy for improving solasodine yields in undifferentiated *in vitro* cultures of *S. eleagnifolium* Cav. The obtained values with some PGR relationships are comparable to those of green fruits of the wild plant.

Through screening and selection it was possible to obtain strains with different productivity along time being the yields constants when using 2,4,5-T as PGR or with high initial values that decreased with time when using 2,4-D as PGR. The cultures of suspended cells were homogeneous, mostly of single cells or small aggregates when using 2,4,5-T for initiation of cultures. The highest yields were attained with NAA (50 μM): kinetin (0.25 μM) and 2,4-D (0.5 μM): BAP (0.5 μM), which were higher than those determined in stems and leaves of the wild type plant. The fact that differentiation is related to the amount of secondary metabolites produced was confirmed after establishing hairy root and transformed stem cultures obtained by infection of S. eleagnifolium Cav. plantlets with A. rhizogenes. Both transformed cultures produced a solasodine yield that was also higher than those of the aerial parts of the wild type plant.

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Chapter 6 Molecular Farming in Plants

Abstract Molecular farming can generally be defined as the production of molecules (proteins, fatty acids) for the pharmaceutical and chemical industries in transgenic organisms (plants, animals, etc.).

Molecular farming in plants has advantageous aspects as biosecurity, they do not bear pathogens for humans or animals, and they do not produce toxins. Also, plant protein synthetic machinery is able to produce complex glycosylated proteins as they have a glycosylation pattern with slight difference respect of that of mammals, and can perform foldings.

When displayed in *in vitro* conditions, molecular farming have the characteristic advantages of that type of culture, mainly the capacity of working under Good Manufactory practices as is required by the pharmaceutical industry. The critical aspects of plants for molecular farming are the different glycosylation patterns respect to mammals, the duration of the productive process, and the relatively low yields.

The approval by the FDA of the first medicine to be used in humans, taliglucerase alfa (ELELYSO®), has give an impulse to this technology but there are some drawbacks to be addressed, particularly related to low yields and regulatory aspects.

Keywords Molecular farming • Recombinant proteins • Plant transformation • Plant glycosylation • *Agrobacterium tumefaciens*

6.1 Introduction

Plants have the unique ability of using solar energy and inorganic compounds to produce biomolecules, some of which are of medicinal interest, as was discussed in previous chapters of this book. Besides, using the available tools of genetic engineering, plants can produce foreign proteins. Molecular farming can be defined as the use of genetically modified organisms (plants, animals) to produce molecules of therapeutic or industrial interest. Although other molecules, as lipids, can be expressed, the term molecular farming is mainly applied to recombinant proteins.

6.2 Recombinant Proteins in Plants

The pharmaceutical industry requires recombinant proteins in sufficient amounts to cover the market demand and to bring a quick response to an epidemic outburst. There is an increasing requirement of those therapeutic proteins, which would not be satisfied in the next few years by the current productive platforms (bacteria, yeasts, or mammal cells). New platforms have demonstrated its potentiality to produce recombinant proteins, as transgenic animal and plants (Thomas et al. 2002; Joshi and López 2005).

The choice of a productive platform depends on the characteristics of the recombinant protein, the market needs, and the production costs among others factors. Each platform has its strengths and weaknesses. Mammal cells in general produce identical proteins as required, but have the risk of harbouring harmful agents (e.g.: prions, pathogens, oncogenes) requiring purification steps that increase costs. Bacteria, which have high production rates, cannot perform the complex post-translational processes typical of eukaryotes (glycosylation, folding) limiting the spectra of recombinant proteins they can express. Also, they require from extra purification steps since they store proteins in inclusion bodies or can produce endotoxins.

Plant cells, being eukaryotes, process proteins as mammals do but with slight variations (e.g., in the glycosylation pattern), and are able to produce complex proteins, including multimeric and glycoproteins (Joshi and López 2005; Stoger et al. 2005; Mascia and Flavell 2004; Daniell et al. 2009). Besides, plants do not harbour pathogens, or produce endotoxins, or include proteins in vesicles. The production of recombinant proteins in plants can be performed in agronomic cultures, in the field, or in in vitro cultures. In the field, scaling up can be achieved by increasing the cultured area with the potential production of hundreds of kilograms of purified protein per year. In the case of in vitro cultures, the scaling up can be achieved increasing the volume of the culture. The disadvantages of plants for producing recombinant proteins are the long extent of the process, the variation of yields and quality of the product, and the difficulty to use good manufacturing (GMP) and good laboratory practices (GLP) in the early stages of production in the field. In addition, there are susceptible to pests and diseases, or can be contaminated by agrochemicals or fertilizers. Furthermore, there are risks of gene transfer to conventional cultures, which requires working under specific regulations for GMOs in the field (Obembe et al. 2011; Xu et al. 2012).

Producing recombinant proteins in *in vitro* cultures has the characteristic advantages of the system (Chap. 4) as well as the capability of producing proteins in GMP and GLP (Hellwig et al. 2004). Also, scaling-up and product purification are simple (Medina-Bolivar and Cramer 2004; Medina-Bolivar et al. 2003).

More than 50 % of the total production cost of a process is related to the extraction and purification of the proteins, which makes critical the operations of down stream processing (DSP). In *in vitro* cultures, the DSP costs can be remarkably reduced if the protein of interest is secreted into the culture medium (Hellwig et al. 2004; Streatfield and Howard 2003; James et al. 2002; Faye et al. 2005).

A bottleneck for the commercial exploitation of plants for producing proteins is their low productivity. To be competitive, the plant system must be optimized at the gene expression, culture development or downstream processing level (Xu et al. 2012).

6.3 Plant Transformation

Plant transformation can be achieved by using direct or indirect natural procedures (Fig. 6.1). Usually, the gene that code for the protein of interest is introduced into the plant genome in a construct that also contain a promoter, a terminator, and different signals that can modulate the expression of the gene in intensity, time and space.

6.3.1 Direct Methods

The most common methods are the physical methods that imply the use of biolistic and electroporation. Chemical methods are PEG, calcium phosphate, and artificial lipids-mediated, among others (Fig. 6.1). Biolistics is one of the most popular direct methods, e.g.: for chloroplast transformation (Bock 2014), for constitutive or in specific-organ expression of the recombinant proteins (Cunha et al. 2011a). These simple methods have the disadvantage of a high rate of cellular damage, and the increased rate of silencing due to multiple copy integration (Egelkrout et al. 2012).

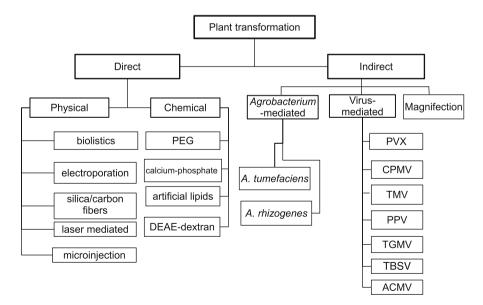


Fig. 6.1 Plant transformation methods

6.3.2 Indirect or Biological Methods

Indirect methods involve the transference of the DNA using *Agrobacterium* or viral vectors.

6.3.2.1 Agrobacterium

Agrobacterium is a natural bacterium with the capability of infecting Dicotiledoneae plants producing the tumoral disease known as the "crown gall" disease (de la Riva et al. 1998). During the infection a fragment of a plasmidic DNA (T-DNA) is transferred to the nucleus of the plant cell. That T-DNA contains two types of genes, the oncogenes (codifying for enzymes involved in the synthesis of auxins and cytokinins responsible for the tumour formation), and the genes codifying for the synthesis of opines. Opines (a condensation of amino acids and sugars) are synthesized and secreted by the gall crown cells, and used by A. tumefaciens as carbon and nitrogen source. Out from the T-DNA are located the genes for the catabolism of opines, the genes involved in the transference of the T-DNA from the bacteria to the plant cells (vir), and the genes involved in the conjugation among bacteria. The T-DNA enters into the plant and integrates randomly in the plant genome by illegitimate recombination. Once integrated, the expression of the oncogenes and of the genes that induce the production of opines is triggered (de la Riva et al. 1998). As a consequence, there is an uncontrolled growth of plant cells an outgrowth of bacteria.

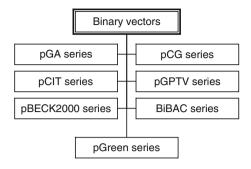
6.3.2.2 The Plasmid Ti

The tumour inducing plasmids (plasmid Ti) are classified according to the induced opines (de la Riva et al. 1998). The most studied are the nopaline/agrocinopine (e.g.: pTiC58 y pTiT37) and the octopine/manopine (pTiB6 y pTi15955). The T-DNA is flanked by 25 bp inverse repeated sequences, the right and left borders (RB and LB respectively) that act as *cis* elements for the transference apparatus. There is a polarity established between them being the RB the first to enter into the plant cell (Gelvin 2003). A remarkable finding was that any foreign DNA placed between the RB and LB can be transferred to the plant cell no matter its origin. That has allowed the construction of vector systems for plant transformation (de la Riva et al. 1998).

6.3.2.3 Vectors

(a) Binary vectors: The introduction of foreign genes in the T region of the *A. tume-faciens* plasmid Ti has some difficulties. First, the plasmid Ti lacks of unique recognition sites for restriction enzymes. Secondly, there is a limit in the size

Fig. 6.2 Main binary vectors in use for plant transformation



the plasmid can bear; DNA fragments of high molecular weight complicate the manipulation (Gelvin 2003). Numerous vectors derived from the disarmed Ti plasmid have been developed (An 1985). In binary vectors two different plasmids are employed, a small plasmid, that has origins of replication both for *Agrobacterium* as *for Escherichia coli*, and do not have its tumour-inducing genes. The plasmid also contain unique restriction sites in the T-region allowing the introduction of the desired genes, promoter sequences, selection markers (antibiotic resistance), directional signals, etc., and are flanked by the right (RB) and left (LB) borders of the Ti-DNA (Gelvin 2003; Hellens et al. 2000). The second plasmid is a helper plasmid that harbours the *vir* genes but do not have the T-DNA region. The main binary vectors are from the series pGA, pCG, pCIT, pGPTV, pBEK2000, binary-BAC (BiBAC) and pGreen (Fig. 6.2).

Each series of vectors has a particular characteristic that makes them useful for plant transformation, e.g., antibiotic resistance genes, particular cloning sites, etc.

Briefly, vectors from the (a) pGA series contain a RK2 ori genes that confer resistance to tetracycline and kanamycine and G418 (*nptII*) and a polylinker site, (b) pCG series contain the pRiHRi (*A. rhizogenes* root-inducing) ori gene, and a *ColE1* ori, (c) pCIT series contain the hygromycin (*hph*) resistance gene and the *cos* site for cloning long DNA sequences, (d) pGPTV series contain marker genes close to the LB, (e) pBECK2000 with synthetic T-DNA borders, genes for phosphinothricin resistance (*bar*), the *p1 Cre/loxP* site recombinase system that allows site-specific excision of marker genes after transformation and the transfer and integration of foreign genes as a single or different T-DNA units, (f) Binary-BAC (BiBac) series, based in the bacterial artificial chromosome vector, low-copy numbers of origenes, a helper plasmid with additional virgenes copies, the elements of the vector are specific to allow transformation with DNA of high molecular weight, (g) pGreen series, contains the ori *pSa*, the *ColE1* ori (from pUC), a *rep A* gene, and multiple cloning sites based on pBlue-Script vector.

(b) Gateway® vectors: the Gateway® cloning system permitted the construction of more rapid and efficient binary vectors. This technology was initially based on phage lambda site-specific recombination (Hartley et al. 2000; Karimi et al. 2002). The phage genome integrates into *E. coli* genome by recombining its

attP site with the attB site of the bacteria (BP reaction); as a result phage genome is flanked by the attL and attR sites. The reaction is reversible (LR re-action). The manufacturer provides the enzymes needed for performing both reactions: BP clonase (phage integrase, Int, plus E. coli integration host factor, IHF) and LR clonase (Int, IHF plus excisionase, Xis). The basis of Gateway® cloning method is the production of a recombinant DNA by means of the att sites and the clonases. There are numerous binary vectors compatible with the Gateway® cloning methodology that can be used as destination vectors (Karimi et al. 2007). The Multisite vectors further developed permitted the recombination of DNA fragments within certain size limits in a single recombination step (Cheo et al. 2004; Karimi et al. 2005; Magnani et al. 2006). Some Gateway compatible binary vector series (pGWB) were made with intermediate plasmids pUGWs, based on pBI plasmids, or pPZP plasmids. For promoter swapping a R4 Gateway binary vector (R4pGWB) series was constructed (Tanaka et al. 2012).

The MultiRound Gateway technology, with two different entry vectors that can sequentially deliver multiple DNA fragments into a Gateway-compatible destination vector, allow stacking multiple DNA fragments (Chen et al. 2006). An improved version of the last one was developed introducing a transformation-competent artificial chromosome-based destination vector and a recombination deficient *Agrobacterium* strain. The resultant vector let introduce up to eight genes placed on a single destination vector, besides other sequences as selection markers, scaffold attachment regions, etc. The inserted transgenes were stably expressed for at least two generations (Buntru et al. 2013).

(c) Co-integrated vectors: they are not commonly in use because they require of long homologies between Agrobacterium and E. coli being less efficient than binary vectors. They are engineered using a Ti-plasmid (SEV-series with a kanamycine resistance gene, pGV series, with a segment of pBR322), intermediate vectors to allow the transference of high-molecular weight DNA sequences, and a helper vector. The resulting vector contains vir genes, a foreign DNA sequence, selectable markers to plants and bacteria, and LB and RB.

6.3.2.4 Viral Vectors

Viral vectors are attractive for their ease and simple manipulation. They are classified in (a) epitope presentation systems, with the peptide displayed in the viral surface, and (b) polypeptide expression systems, with the transgene usually expressed as a non-fused polypeptide in infected cells. In the first group are vectors derived from the cowpea mosaic virus (CPMV), tobacco mosaic virus (TMV), tomato bushy stunt virus (TBSV), plum poxvirus (PPV), and alfalfa mosaic virus (AIMV). In the second group, are vectors derived from TMV, potato virus X (PVX), PPV, TBSV, CPMV (Cañizares et al. 2005). Also, viral vectors were developed based on the geminivirus tomato golden mosaic virus (TGMV) (Hong et al. 2004).

6.3.2.5 Promoters

Gene regulation is mediated by signals placed contiguously (*cis*-acting) or not (*trans*-acting) to the encoding-sequences. Promoters generally appertain to the first category of modulators; usually they are binding sites for transcription factors (TFs), which are trans-acting modulators of gene-expression. They can be only active in a particular species, genus or family (homologous) or in different species or even kingdoms (heterologous).

For plant transformation, promoters generally in use can be (a) constitutive, generally heterologous, which direct expression in the whole plant without being conditioned by exogenous or endogenous factors, (b) tissue specific, usually homologous, that drive gene expression to a particular tissue or stage of plant development (e.g., roots, seeds, parenchyma, etc., (c) inducible, which are conditioned by exogenous stimuli, as biotic and abiotic factors (light, temperature, oxygen level, chemicals, wounding) allowing gene modulation by antibiotics, metals, herbicides, etc., and (d) synthetic promoters, tailored with elements of different promoter regions (Fig. 6.3).

Other regulatory systems are based on trans-activating proteins that can be used in combination with promoters. In eukaryotes, promoters contain several elements, some of them present in the majority of promoters: the CAAT or the AGGA box, a consensus sequence –80 bp from the start point, that increase the promoter strength; the TATA box, placed 25 bp upstream of the start point, usually surrounded by GC rich sequences, that is the place of binding of RNA polymerase II and some TFs; a GC box, rich in guanidine (G) and cytosine (C), usually found in multiple copies in the promoter region, in general surrounding the TATA box; and a CAP site, which is the transcription initiation sequence (+1). Out from the promoter sequence, enhancer sequences can be added upstream or downstream-from the promoter, they enhance promoter activity by binding some TFs, also, in some cases; they can confer tissue specific or stage-specific gene expression (Fig. 6.3).

(a) Constitutive promoters: they are the most popular promoters at least for research. The main reasons are that they are strong promoters, which mean that

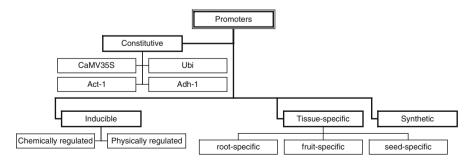


Fig. 6.3 Classification of promoters for plant transformation

the level of protein expressed is usually high, and that the distribution of the protein expressed is ubiquitous during all stages of plant development.

- CaMV 35S: promoter of the Cauliflower Mosaic Virus is a very strong promoter, highly efficient in Dicotiledoneous.
- Ubi: promoter that controls the expression of the *Ubi-1* and *Ubi-2* genes encoding ubiquitin in maize. A relevant region contained in *Ubi* is two overlapping sequences, heat shock inducible, located −214 to −204 from the start site.
- Act-1: in the 5' region of rice actin-1 gene it has two relevant regions, a 38 bp poly (dA-dT) element located from -245 to -152, which is the place of binding for trans-acting positive regulators of Act-1, and a CCCAA pentamer repeats, from -300 to -260, involved in the negative regulation.
- Adh-1: promoter of maize alcohol dehydrogenase. The anaerobic regulatory elements (ARE) of the promoter and the first intron of Adh-1 gene sequence are combined in one promoter named EMU that also contains enhancer elements from the octopine synthase (OCS) gene from *A. tumefaciens*, and a TATA box.
- (b) Tissue-specific promoters: they control gene expression in a tissue-dependent mode or according to the plant development phase. There are numerous inducible promoters in use. In general they are homologous since the modulation must be carefully adjusted. Some examples are for:
 - Seed-specific: beta amylase promoter, barley hordein gene promoter.
 - Root-specific: tobacco RD2 gene promoter.
 - Ovary-specific: tomato pz7 and pz130 gene promoters.
 - Fruit-specific: banana TRX promoter, melon actin promoter.
- (c) Inducible promoters: their main characteristic is that they allow that the expression of a particular gene (or genes) can be turned on or off under certain conditions. They can be chemically or physically regulated.

Chemically regulated: their activity is regulated by different chemicals as alcohol, tetracycline, metals, and steroids. Those chemicals are not plant metabolites, but must be specific for the gene under study, no toxic for the plant and easily manipulated. Into this group are the pathogenesis regulated (PR) promoters, induced by salycilic acid (SA), ethylene and benzothiadiazole (BTH), chemicals that are liberated by the plant during pathogenesis. Usually BTH, which act systemically and has a long-term effect, is best tolerated for plants than (SA), which acts in the site of application.

Physically regulated: they are induced by environmental factors as temperature (cold or heat-shock induced), light (e.g.: from pea or myxobacterium), salt stress, water availability, etc. Some examples are the light-responsive elements in the ribulose-1,5-biphosphate carboxylase-oxygenase and chalcone synthase gene promoters.

(d) Synthetic promoters:

They are tailor-made by combining sequences from other promoters they must contain at least a TATA box, a CAP site, and a CCAAT consensus sequence.

6.3.3 Stable Transformation

In 1983 Herrera-Estrella et al. reported the functional expression of a foreign gene after engineering a T-DNA replacing the *vir* genes for the gene of the heterologous protein. The construct also carried a promoter, a terminator, and a gene that codified for a selection marker. That was the starting point for expressing recombinant proteins using *Agrobacterium* as a vector. Since then, a variety of technologies have been developed to attain the expression of genes in plants with high yields (Fig. 6.4).

6.3.3.1 Nuclear Transformation

The gene for the protein of interest is usually under the control of a strong constitutive promoter, as the promoter of the cauliflower mosaic virus (CaMV35S). In that case the protein is expressed in the whole plant but, usually is extracted from leaves. In the cell, the recombinant protein can be targeted to a specific sub-cellular location, as the endoplasmic reticulum, the cytoplasm, etc., by the addition of the proper signals.

Tobacco is one of the more employed species, its transformation is not complicated, produces a high amount of biomass (more than 30 t per acre), and is not in the food chain (Tremblay et al. 2010). Besides, several tobacco varieties with low nicotine and alkaloid content have been developed, which overcome the potential toxicity of the products (Menassa et al. 2001). Other species with good leaf development as *Lactuca sativa*, *Medicago sativa*, *Trifolium* sp. are also used. Two limitation of expressing recombinant proteins in leaves are their short shelf life, which requires an immediate post-harvest processing to assure the stability and quality of the protein, and the susceptibility to environmental factors (biotic and abiotic), which may affect the yields.

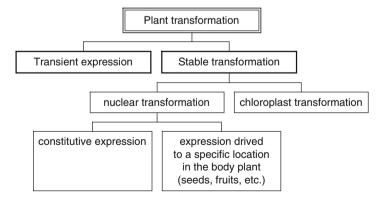


Fig. 6.4 Proteins can be expressed in plants in two ways: transiently (e.g. by Agroinfiltration), or by stable transformation using the protein synthesis machinery of the nucleus or chloroplasts

Fruits, as tomato (*Solanum lycopersicum*) has also been used to produce PMPs (Mason et al. 2002), e.g.: an antigen fusion protein, F1-V, against *Yersinia pestis*. Hyroponic transgenic cultures were grown in a greenhouse with continuous harvest of fruits. The estimated maximal antigen production was about 293 mg m⁻² per year, which can be improved ameliorating the environmental conditions and culture practices (Matsuda et al. 2009).

The recombinant proteins constitutively expressed in plants include antibodies, vaccines, citoquines, growth hormones and industrial proteins (Benchabane et al. 2008; Sharma and Sharma 2009) (Table 5.1). The first clinical assay for a recombinant protein was a variant of the Guy's13 secretor antibody expressed in tobacco (Ma et al. 1998).

6.3.3.2 Chloroplast Transformation

Gene integration, by homologous recombination, in chloroplasts produces hundreds of copies of the transgene and consequently high recombinant protein yields were attained (Bock 2014; Gao et al. 2012; Day and Goldschmidt-Clermont 2011; Daniell et al. 2005; Gleba et al. 2005). Chloroplasts perform relevant post-translational modifications, the system is devoid of gene silencing, and has the advantage of the maternal inheritance that reduces the possibility of transgene transmission through pollen, and allows to stack multiple transgenes in operons and co-express them from a single promoter as a polycistronic mRNA (Bock 2014; Thyssen et al. 2012).

Some drawbacks are the expression limited to non-glycosylated proteins, protein instability, and the low expression levels in non-green tissues.

Enzymes, antibodies, antigens and other proteins of interest for the pharmaceutical industry (e.g.: human serum albumin) have been expressed in plastids (Fernández-San Millán et al. 2003; Clarke et al. 2011; Bock 2014).

6.3.3.3 Expression in Seeds

The main advantage of expressing proteins in seeds is their stability during storage at room temperature with a minimal lack of protein activity (Boothe et al. 2010). In this case, protein expression is directed to seeds through the appropriate sequence-signal. In seeds, proteins, protected from proteolytic degradation, attain high expression levels (7–10 % TSP). Most of the seeds used to express recombinant proteins belong to species in the food chain (Oryza sativa, *Triticum aestivum*, *Glycina max*, *Zea maïs* and *Hordeum vulgare*), which demands strict protocols and documenting each step of the process (Ramessar et al. 2008; Ramessar et al. 2009). Some of the proteins expressed in this way are the functional recombinant human growth hormone and the coagulation factor IX in soybean seeds (Cunha et al. 2011a, b).

The extraction of proteins from seeds has been improved by the fusion of the recombinant protein to oleosines that accumulate in oil bodies. This technology has allowed the production of recombinant human insulin in transgenic safflower (Univ. of Calgary).

6.3.4 Transient Expression

Proteins can be transiently expressed, with no need for stable integration of the transgene. The foreign genes are delivered by vacuum infiltration in the mesophylle of leaves. The vectors can be *Agrobacterium* spp. (Kapila et al. 1997), viral vectors (Verch et al. 1998), or a combination of both (magnification) (Gleba et al. 2005). In general, the production of recombinant proteins started 24 hs post-infection and continues for several days (*Agrobacterium* mediated) to several weeks (virus mediated) (Gleba et al. 2005).

Initially, transient transformation was used to test the efficiency of the constructs designed for expressing genes and for validating the activity of newly expressed recombinant proteins (Circelli et al. 2010; Whaley et al. 2011). Then, it became attractive for producing biopharmaceuticals due to their high protein yields and to not generate a GMO (Circelli et al. 2010; Sheludko 2008). Another advantage of this system is that it allows the rapid co-expression of multiple genes (Huang and Mason 2004; Medrano et al. 2009).

Transient expression was performed in several species, e.g.: *N. benthamiana*, *Arabidopsis*, *Solanum tuberosum*, *Phaseolus*, *Lactuca sativa*, etc.

Some authors have found that with *Agrobacterium* yields was between 0.1 a 180 μ g g⁻¹ (Medrano et al. 2009). In general, protein yields are between 4 to 20-fold higher than by stable transformation (using the CaMV35S promotor) (Medrano et al. 2009). With viral vectors the yields are higher than with *Agrobacterium*, e.g.: 5 mg g⁻¹ for GFP (green fluorescent protein) (Marillonnet et al. 2004). However, the expression usually is after the 14th day of infection, which complicates the stability of the recombinant protein.

Magnification is a shorter process, with quite higher protein yields, versatile, with no wild type virus generated (Gleba et al. 2005). By agroinfiltration, the HIV-1 *Nef* protein was expressed in *N. benthamiana* leaves testing also the effect of genesilencing viral suppressors on yield (Circelli et al. 2010). The highest *Nef* yield (1.3 % of total soluble protein) was attained when the P19 of Artichoke Mottled Crinckle virus was co-expressed, which correlates with a fall in the amount of Nef-interfering RNAs.

An interesting approach was the use of a transient large-scale plat-form to a fast reaction to a pandemic outbreak of influenza (D'Aoust et al. 2010). The H5 virus-like protein (VLP) was expressed by agroinfiltration in *A. thaliana* at large-scale (1,200-1,500 plants per week), obtaining approximately 25 kg of leaf biomass at the 6th day post-infiltration. Using this technology the research group, from the Medicago Inc. company, has tested an experimental vaccine against a novel strain (A/H1N1) that appeared in 2009, proved its immunogenicity in mice, and demonstrated its efficacy and speed of response (Landry et al. 2010; D'Aoust et al. 2010) with clinical trials are in progress. In 2013 they have developed a plant-based Rotavirus VLP vaccine candidate using the same platform. Some companies are using this platform for producing commercial proteins, e.g. Genaware produces α -tricosantine and acid lyzosomal human lipase, MagnIcon produces hepatitis B antigen and viral Norwalk-like particles virus and F1 and V *Yersinia pestis* antigens,

and by Geminivirus technology the heavy and light chains of the monoclonal antibody 6D8 IgG–like against the Ebola GP1 virus are produced. The Launch expression system combines the genome of a plant viral vector with the *Agrobacterium* binary plasmid. The expression of the recombinant influenza H5HA-1 protein attained a yield of $60 \mu g g^{-1}$ of fresh leaves (Yusibov and Mamedov 2010).

Those systems are used at industrial scale in the Fraunhofer Center for Molecular Biotechnology (Newark, DE), Medicago Inc (Quebec, Canadá), Texas AandM (College Station, TX) and Kentucky BiProcessing LLC (Owensboro, KY). Terrasphere have developed a high-density hydroponic system that can produce high amounts of recombinant proteins.

6.4 In vitro Cultures

In vitro cultures (suspended cells, hairy roots) have the advantage of managing the process in controlled environmental conditions under GMP and GLP. Production is faster than in agronomic cultures, and down stream processing is easier and cheaper specially when the product is recovered from the culture medium. Production can be performed in undifferentiated (suspended cells) or differentiated (hairy roots) cultures. A variety of recombinant proteins have been expressed such as antibodies, antigens, enzymes, etc.

6.4.1 Cell Suspension Cultures

Numerous proteins have been expressed, mainly in *N. tabacum* strains BY-2 (Bright Yellow-2) and NT-1 (*N. tabacum*-1) which are easily transformed with *Agrobacterium*, have a fast and robust growth, with the ability of synchronizing their cell cycle. Also, *N. tabacum* cv. Xanthii, carrot, rice, etc. have been used (Terashima et al. 1999). The yields or recombinant protein attained are variable, the low levels were attributed to protein degradation by proteases or the adsorption of proteins onto the surfaces of the culture vessels (Doran 2000). Other proteins produced in cell suspension cultures arte factor XIII-A domain in tobacco (Gao et al. 2004), human interleukins in tobacco (Magnuson et al. 1998; Kaldis et al. 2013). Besides tobacco, *N. benthamiana*, *Arabidposis thaliana*, rice, carrot, and other species have been used for producing recombinant proteins in cell suspension cultures.

6.4.2 Hairy Roots

Hairy roots are obtained by infecting plants with *A. rhizogenes* (see Chap. 4). *A. rhizogenes* bears the Ri plasmid that induces root formation in the plants that infects. The integration of the T-DNA plasmid in the plant genome results in a

differentiation and development of neoplasic roots, hairy roots, in the infection sites. Hairy roots are characterized by an indefinite growth with high genetic stability. Hairy roots, cultured in controlled conditions, produce recombinant proteins in GMP. Besides, it is possible the extracellular secretion or rhizosecretion of the protein, allowing a less expensive recovery in a well defined culture media with low protein content.

Recombinant antibodies, enzymes, antigens, growth factors, immunomodulators, interleukine-12, human acetylcholinesterase, etc. have been expressed in hairy roots (Wongsamuth and Doran 1997; Woods et al. 2008).

A limitation of hairy roots is the filamentous, highly branched morphology that difficult their culture in classical bioreactors. To overcome that inconvenient, new bioreactor designs were developed. An example is the mist reactor that offers a low hydrodynamic stress with high volumetric oxygen transference levels (Weathers and Giles 1988).

6.5 Plant Glycosylation

Plants can manage protein synthesis performing modifications in a similar way than mammal cells with several differences although the sequence-specificity is not always conserved (Gomord and Faye 2004). Also, N-glycosylation differences could represent a severe limitation on the use of plant-made pharmaceuticals that triggered abundant work on the field (Bardor et al. 2006), O-glycosylation, which has been less studied (Daskalova et al. 2010).

N-glycosylation usually affects protein stability, solubility, folding, and biological activity (Bosch et al. 2013). The first steps of protein synthesis, that take place in the endoplasmic reticulum, are similar in plants as mammals; the oligosaccharide precursor on the nascent protein backbone is transferred to a specific residue of asparagine. The protein follows its path through the ER and Golgi where suffers the removal or addition of sugar residues. The process in plants and mammals differs when the nascent proteins is transferred to the Golgi apparatus. In plants, a β -1,2-xylose is linked to a core mannose residue, and a α -(1,3) fucose is linked to the proximal N-acetylglucosamine. Also, plants lack the terminal β -(1,4) galactose residues (Fig. 6.5). In general, plant-derived proteins are a heterogeneous N-glycan group, with a few exceptions, e.g., the monoclonal C5-1 antibody produced in alfalfa (Bardor et al. 2003; D'Aoust et al. 2004).

Plants have been engineered in several ways to generate recombinant glycoproteins with a customized N-glycosylation pattern (Castilho et al. 2011). The enzymes responsible of the addition of residues typical of plants were knocked out, or the expression of the human glycosyltransferase and the introduction of sialic acid were engineered (Castilho et al. 2012) for their effect on protein biological activity and half-life (Abranches et al. 2005).

Additionally, N-glycosylation can be modified *in vitro*, e.g.: the β -(1,4) -glycosyltransferase from bovine milk was added to transgenic alfalfa plants (Bardor et al. 2003) and also sialic acid (Raju et al. 2001).

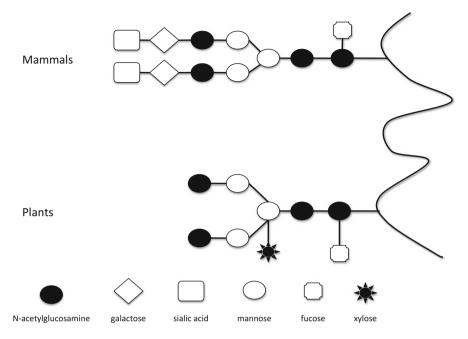


Fig. 6.5 Glycosylation pattern of plants and mammals

In addition, gene disruption by homologous recombination was performed to design a double knockout strain that lacks the two plant-specific sugar residues, fucose and xylose, implicated in allergic immune responses (Lerouge et al. 2000; Koprivova et al. 2004).

As for O-glycans, they are primarily attached to hydroxyproline and serine residues in plant glycoproteins. In mammalian cells, O-glycans are mucin type O-linked glycans, which are synthesized in the Golgi in a succession of steps, independently of the consensus motifs. It was demonstrated that plants can be engineered to express a complex O-glycoprotein, LTBMUC1 (E. coli enterotoxin B subunit: H. sapiens mucin 1 tandem repeat-derived peptide fusion protein), with the mammal characteristic O-glycosylation. LTBMUC1 was expressed in N. benthamiana by stably and transient transformation using A. tumefaciens that also co-express human GalNAc-T2, the Caenorhabditis elegans UDPGlcNAc/UDPGalNac transporter, and Yersinia enterocolitica UDP-GlcNAc 4-epimerase required for the GAlNAcglycosylation typical of mammal cells. LTBMUC1 also appeared decorated with plant-specific glycans attached to the hydroxyproline residues (Daskalova et al. 2010). Recent studies have shown that plant-specific Hyp-O-glycosylation might be an alternative to PEGylation to increase the serum half-life of human therapeutic proteins; however, it is necessary to perform an analysis of the possible induction of immunogenicity and/or allergenicity in humans (Gomord et al. 2010).

6.6 Plant-Made Proteins for Health

There are numerous reports about expression of recombinant proteins in plants (Ahmad et al. 2012). The most used species are *N. tabacum*, *A. thaliana*, *Oryza sativa*, tomato, *Medicago sativa*, *Glycina max*, *S. tuberosum*, *Zea maïs* (Twymann et al. 2003; Fischer et al. 2004). Technical advances have permitted the transformation of a large variety of plant species including non-conventional species as *Medicago trunculata*, which produces more homogeneous glycans structures (Abranches et al. 2005).

6.6.1 Antibodies

Antibodies are one of the more relevant groups of biopharmaceuticals, with a growing demand that might rapidly not be covered by the platforms in use. Hiatt et al. (1989) reported the expression of an antibody in plants for the first time. Initially, the heavy (H) and light (L) chains of the immunoglobulin were cloned separately. Then the resultant transformed plants were sexually crossed; the progeny contained some transgenic plants that expressed the assembled chains as a functional antibody. Later on, the cloning of the genes for both chains in a single event was reported, producing a plant that expresses the whole functional antibody (Table 6.1). Functional antibody fragments are also expressed, the fragment antigen binding (Fab), containing one of the two identical combining sites of the immunoglobulin, the antibody single bivalent fragments F(ab')2 containing the two combining sites, fragments consisting of only the variable regions of the L and H chains (Fv), that retain the antigen binding capacity, single-chain variable fragments (scFv) consisting of the VL and VH domains linked by a flexible peptide, maintaining the binding capacity (Seddas-Dozolme et al. 1999; Eeckhout et al. 2004; Galeffi et al. 2005), and single-domain antibodies (VHH) from camelids (Marconi and Alvarez 2014). Secretory antibodies (IgA) are also expressed (Larrick et al. 2001).

Table 6.1	Selected examples of an	tibodies expressed in plants	

Antibody	Plant species	Reference
C5-1	Medicago sativa	Bardor et al. (2003)
sIgA anti-S. mutans	N. tabacum	Ma and Hein (1995)
Human anti-Rhesus D IgG ₁	Arabidopsis	Bouquin et al. (2002)
Anti-CD4 and anti-CD28 scFv	Triticum estivum (cv. Westonia)	Brereton et al. (2007)
MAK33	N. tabacum, S. tuberosum	De Neve et al. (1993), De Wilde et al. (2002)
Guy's 13	N. tabacum	Wongsamuth and Doran (1997)
C5-1	N. benthamiana	Sainsbury and Lomonossoff (2008)
LO-BM2	N. tabacum	De Muynck et al. (2009)
Caro-Rx	N. tabacum	Fischer et al. (2003)

6.6.2 Vaccines

Plants also express immunogen antigens that will be used for formulating experimental vaccines (Table 6.2). The production of plant edible vaccines was proposed in the late '1980s, but it took several years to finally prove the concept (Haq et al. 1995; Mason and Arntzen 1995). Currently, there are some vaccines with plant made antigens in its formulation in clinical trials (Ahmad et al. 2012; Franconi et al. 2010), to be used as an edible, parenterally or topically administered vaccine (Giorgi et al. 2010).

The generation of transgenic plants by plant nuclear transformation has successfully produced mucosal vaccines against cholera, Norwalk virus, hepatitis B, and foot-and-mouth disease. The cholera toxin B subunit, the first plant-derived vaccine arising from plastid transformation, accumulates to 4.1 % total soluble protein in tobacco leaves (Daniell et al. 2001; Walmsley and Arntzen 2003).

Also, the diphteria toxin (DT), tetanus fragment-C (TetC) and the non-toxic S1 subunit of pertussis toxin (PTX S1) antigenic proteins have been expressed in low-alkaloid tobacco plants and carrot cell cultures. The coding sequences were placed, under the control of the strong promoters RbcS1 (tobacco) or CaMV35S (carrot), into the binary vector pBINPlus having the *nptII* gene for kanamycine selection. The antigens were produced in tobacco leaves or in optimized carrot cell suspension cultures, after extraction and purification they were used to formulate a vaccine that was injected to BALB/c mice. A strong antigen-specific serum antibody response was triggered after exposition to a commercial native diphteria, tetanus or pertussis toxoid (Brodzik et al. 2009).

Tomato was tested as an edible vaccine against malaria (Chowdhury and Bagasra 2007), lettuce against the *E. coli* heat-labile toxin B subunit (Martínez-González et al. 2011), rice against the roundworm *Ascaris suum* (Matsumoto et al. 2009).

Recombinant antigen	Plant species	Reference
Hepatitis B surface antigen	N. tabacum	Kostrzak et al. (2009)
	S. tuberosum	
Hepatitis B surface antigen	Cherry, tomato	Gao et al. (2003), Thanavala et al. (2005)
TetC (Tetanus vaccine antigen)	N. tabacum	Tregoning et al. (2004)
Bacillus anthracis protective antigen	N. tabacum	Watson et al. (2004)
Hepatitis B surface antigen	Banana	Kong et al. (2001)
Hepatitis B surface antigen	N. tabacum	Kostrzak et al. (2009)
Anthrax protective antigen	N. Tabacum	Brodzik et al. (2009)
	Daucus carota	
DTP subunit vaccine	M. sativa	Brodzik et al. (2005)
ESAT6:Ag85B tuberculosis antigens	A. thaliana	Dorokhov et al. (2007)

Table 6.2 Selected examples of antigens expressed in plants

A complete review about plant-made vaccines was published by Awale et al. (2012). Information about the use of plant-made immunogens for developing veterinary vaccines is presented in Chap. 7.

6.6.3 Other Pharmaceutical Proteins

Besides antigen and antibodies, protein allergens, enzyme, enzyme inhibitors, coagulation factors, cytokines, and hormones were expressed in plants (Benchabane et al. 2008) (Table 6.3). Peptides, as the synthetic antimicrobial peptide D4E1 were expressed in tobacco (Cary et al. 2000). Crude extracts resulted inhibitory for *Aspergillus flavus* and *Verticillium dahliae*, while transformed plants were resistant to *Colletotrichum destructivum*. Also, the HPV16 E7 and HPV16 L2 peptides were transiently expressed in *N. benthamiana*. A synergistic interaction was found using viral PVX-based expression vector pGR106 with an increase in the level of the recombinant peptides expressed (Cerovská et al. 2008).

Human somatotropin has been observed to accumulate to 7 % total soluble protein in plastid transformation, 300-fold greater than in nuclear-transformed tobacco (Staub et al. 2000), whereas human serum albumin accumulates to 11.1 % total soluble protein, 500-fold higher than in nuclear transformed leaves (Fernández-San Millán et al. 2003).

The human coagulation factor IX (hFIX) was expressed, using biolistics, in *Glycine max* seeds attaining amounts up to 0.23% ($0.8~g~kg^{-1}$ seeds) of total soluble protein content. The recombinant (hFIX) remained stable and functional for up to 6 years stored at room temperature (Cunha et al. 2011a).

Recombinant antigen	Plant species	Reference
Serum albumin	N. tabacum	Peter et al. (1990)
α-Amylase	M. sativa	Austin et al. (1995)
Human Protein C	N. tabacum	Cramer et al. (1996)
LT-B (heat-labile toxin B)	Zea maïs kernels	Chikwamba et al. (2003)
Avidin	Zea maïs	Hood (2002), Hood et al. (2002)
Human lactoferrin	N. tabacum	Jeffrey et al. (2000)
Tyrosin	Zea maïs	Woodard et al. (2003)
α1-antitrypsin	Oryza sativa	McDonald et al. (2005)
Tricosanthin-α	Trichosanthes kirilowii	Lei et al. (2006)
Hirudin from Hirudo medicinalis	Canola	Demain and Vaishnav (2009)
UreB (urease) protein	Daucus carota	Zhang et al. (2010)
Salmo salar (SasalFN-α1) protein	S. tuberosum	Fukuzawa et al. (2010)
	O. sativa	
GM-CSF	N. tabacum	Kim et al. (2004)
Human interleukin-10	O. sativa seeds	Fujiwara et al. (2010)

Table 6.3 Selected examples of recombinant proteins expressed in plants

6.6.4 Strategies for Increasing Yields

Frequently, a drawback of plants as a platform for recombinant protein production is the low yields. Therefore, the challenge is to optimize the yield and quality of the protein produced. An exhaustive review can be found in Egelkrout et al (2012).

Briefly, the actions for increasing recombinant protein yields can be taken at three different stages:

6.6.4.1 Plant Cell Level

- (a) transcriptional: by selecting promoters that best fit to our needs (strong, inducible), use of sequences that modulate gene expression (enhancer, activators, suppressors) (Dorokhov et al. 2002; Kasuga et al. 2004; Singer et al. 2010);
- (b) translational: Optimization of 5'- and 3'- untranslated regions (UTR), codon design (e.g. codon vegetalization) (Sugio et al. 2008);
- (c) post-translational: directing the expression and accumulation of the protein in a subcellular compartment with low levels of overall proteolytic activity (ER, chloroplasts, etc.) (Gomord et al. 1997; Ma et al. 2003; Chou and Shen 2010), directing the protein to the secretor pathway to collect it from the culture medium (e.g.: in *in vitro* cultures) (Hellwig et al. 2004; Komarnytsky et al. 2006; Lienard et al. 2007; Benchabane et al. 2008), co-expressing the protein with protease inhibitors (Faye et al. 2005; Michaud et al. 2005; Komarnytsky et al. 2006), or expressing the recombinant protein as a fusion protein with a stable and highly expressed peptide (Nygren et al. 1994; Stahl et al. 1997).

6.6.4.2 Optimization of the Environmental Conditions

The environmental conditions can be ameliorated by driving the accumulation of the recombinant protein to a determined more favorable organ (green or senescent leaves, seeds, tubers, roots), by the addition of protease inhibitors (EDTA, leupeptin, PMSF, etc.) to avoid the action of proteases present in the plant extract and by optimization of the culture conditions in *in vitro* cultures (Benchabane et al. 2008; Stoger et al. 2005; Michaud et al. 1998; Artsaenko et al. 1998). Another common strategy is the addition of protein stabilizing agents (gelatin, polyethylene glycol, polyvinylpyrrolidone, albumin) to the culture medium (Doran 2006b; Soderquist and Lee 2005).

Addition of stabilizers: additives such as gelatin and polyvinylpyrrolidone (PVP) appear to be effective (Magnuson et al. 1996; Wongsamuth and Doran 1997; Doran 2006a etc.). The addition of PVP, human serum albumin showed certain limitations at upstream process level, such as foam formation (HAS), and at downstream process level, by a reduction of the binding efficiency on chromatography columns (PVP).

- Osmotic agents (mannitol, inositol), that inhibit cell disruption, have also influenced positively the accumulation of recombinant proteins (Lee et al. 2002; López et al. 2010).
- Coating agents (e.g.: Pluronic F127), the addition of such agents that avoid the
 adsorption of the recombinant protein to the vessels surfaces has demonstrated
 that increase the yield of some recombinant proteins (Doran 2006b).
- Oleosins are the main membrane proteins from oil bodies, they are alkaline and hydrophobic proteins with an amphipathic N- and C- termini, and a central hydrophobic domain. The hydrophobic domain is embedded in the phospholipid monolayer that surrounds the oil body, and the amphipathic domains are exposed to the surrounding environment (Bhatla et al. 2010). Oil bodies have the property of being easier to be separated from other cellular compartments and contaminating proteins by floating centrifugation (Ling 2007). The expression of recombinant proteins, fused to oleosines, in the surface of oil bodies is a strategy proposed to simplify the down stream processing. Some recombinant proteins have been expressed fused to oleosines such as hirudine, a specific thrombin inhibitor, that was expressed in *Brassica napus* and *B. carinata* (Parmenter et al. 1995; Chaudhary et al. 1998), a recombinant human precursor of insulin (Des-B30) and insulin were expressed in *Arabidopsis* (Nykiforuk et al. 2006; Markley et al. 2006), epidermal growth factor in *Arabidopsis* (Moloney and Van-Rooijen 2006), and also several antigenic peptides (Deckers et al. 2004).

6.6.4.3 Optimization of Large-Scale Processes

The selection of the bioreactor design is crucial (conventional, plastic-sleeves, etc.), as well as the mode of operation (batch, fed-batch, continuous), and the removal of the recombinant protein from the culture medium (if it is secreted) or from the biomass (if it is retained at subcellular level) (Doran 2000).

A remarkable aspect of conducting a productive process in a bioreactor is that it could be conducted following the regulatory requirements for the production of recombinant protein for therapeutics.

Down Stream Processing

When the protein is retained into the biomass, e.g., retained in the ER, the protein has to be extracted, a step that complicates the purification process. On the contrary, if the protein is targeted to the secretory pathway its recovery from the culture medium is easier and therefore less expensive (Baur et al. 2004). The stability of the recombinant protein also determines the strategy to be used, in some occasions the addition of stabilizers to the culture medium render highest yields (PVP, gelatin, etc.).

Also, the combination of ultrafiltration and chromatography was employed to purify a recombinant human monoclonal antibody (anti *Pseudomonas aeruginosa*

Level		Strategy	
Plant cell	Transcription	Strong, and/or inducible promoters	
		Enhancers, activators and repressors	
	Translation	Optimization of 5'- and 3'- UTR (untranslated regions)	
		Codon design	
	Post-translation	Driving to sub-cellular compartments, co-expression with protease inhibitors, cofactors. Expression as fusion proteins with a stable and highly expressed peptide	
In vitro		Optimization of the culture medium	
cultures		Addition of protein stabilizers	
		In situ extraction of proteins	
Bioreactor		Selection and improvement of bioreactor design	
		Culture strategy (batch vs. fed-batch vs. continuous culture)	
		Secretion into the culture medium	

Table 6.4 Most common strategies employed to increase recombinant protein expression

serotype O6ad immunoglobulin G1) with a high degree of removal of impurities and the complete recovery of the antibody. The authors included a two-stage cascade ultrafiltration process (a 50 kDa module and a 50 or 100 kDa MiniKros hollow fibre module, both operated at a shear rate of 1,800 s⁻¹) followed by a two-step chromatographic procedure (Mayani et al. 2013).

To facilitate the isolation and purification of the recombinant proteins by a Ni NTA affinity chromatography, a His6-tag sequence can be included in the construct.

Other strategy is to produce elastin-like polypeptides fusion proteins (ELPylation) to take advantage of the temperature-dependent, reversible aggregation/precipitation of ELPs and avoid tricky and expensive chromatographic steps, e.g.: for the expression of spider silk protein in the ER of tobacco and potato (Scheller et al. 2004; Floss et al. 2009).

Table 6.4 summarizes some of the most common strategies employed to improve plant-made protein yields.

6.7 Concluding Remarks

The production of recombinant proteins for medical purposes in plants is undoubtedly an alternative to the classical production plat-forms. However, their use is not yet commercially extended. The approval of taliglucerase alfa (ELELYSO®) is promissory but there are some drawbacks that have to be addressed.

Each recombinant protein is a particular challenge, thus generalization is not strictly possible making necessary to balance several aspects such as the plant species that will express the protein, if a the best strategy is a transient or a stable expression, if the protein will be expressed in the whole plant or in a particular organ or even in *in vitro* cultures, etc.

A considerable amount of functional proteins of animal origin have been expressed in plants including antibodies, antigens, enzymes, blood proteins, citoquines, growth factors and growth hormones (Davies 2010; De Muynck et al. 2010; Xu et al. 2012).

The plant-made proteins resulted functional in most of the cases because plants can perform the adequate folding, establishment of disulfide bonds, subunit assembly, proteolytic cut, and glycosylation.

Antibodies produced in plants were the focus of study for the significant cost reduction that could be attained in the case that the productions in plants were successful (De Muynck et al. 2010). In fact, it is considered that plants are the sole viable platform for producing recombinant secretory antibodies (IgAs) (Paul and Ma 2011).

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Chapter 7 The Antibody 14D9 as an Experimental Model for Molecular Farming

Abstract The catalytic antibody 14D9 is an IgG1-like murine antibody that catalyzes the highly enantioselective protonation of enol-ethers. It was utilised as experimental model for studying the expression of an antibody in tobacco.

The ability of *Nicotiana tabacum* to express the whole antibody was confirmed. Also, *in vitro* cultures of *N. tabacum* were established and their ability to express the antibody was demonstrated. Attempts to improve the 14D9 initial yields were performed by the addition of a KDEL endoplasmic reticulum (ER) retention signal to the construct, therefore two *N. tabacum* lines were used in all the experiments, one with the secretory variant of the antibody (sec-Ab), and another one that retains the antibody in the ER (Ab-KDEL).

Other strategies tested were the optimization of plant growth regulator balance in the culture medium, and the addition of protein stabilizers, plant cell wall permeabilizers and osmotic agents. Besides, hairy root cultures were established and the conditions to express 14D9 were analyzed.

Comparing the yields obtained in all the platforms and system examined, we can conclude that hairy roots growing in Erlenmeyer flasks and Ab-KDEL cell suspension cultures growing in a 2-l bioreactor gave the highest 14D9 yields.

Keywords Catalytic antibody • 14D9 • *Nicotiana tabacum*-recombinant antibodies • Cell suspension cultures • Hairy roots

7.1 Introduction

Antibodies were among the first heterologous proteins expressed in plants (Hiatt et al. 1989). Soon after plants were engineered to express antibody fragments such as Fab, Fv, scFv, VHH, etc. (Desai et al. 2010; Egelkrout et al. 2012; Marconi and Alvarez 2014a).

As discussed in previous chapters, the production of recombinant proteins in *in vitro* cultures has additional advantages over whole plants. *In vitro*, the whole process can be performed in a shortest period of time, in environmental controlled conditions and good manufacturing and good laboratory practices (GMP and GLP) as is required by the pharmaceutical industry (Hiatt et al. 1989; Horsch et al. 1984; Paul and Ma 2011).

Among the antibodies, the catalytic antibodies are of particular interest for their capability to catalyse chemical reactions with a high regio- and stereoselectivity (Sinha et al. 1993). Furthermore, they can catalyse chemical transformations on demand, even in the case of reactions where no natural enzyme are available, making their production attractive to the chemical industry (Tanaka 2002).

In general, catalytic antibodies are produced by chemical synthesis or semi-synthesis (Hasserodt 1999; Reymond 1999). They can also be expressed as recombinant antibodies in bacteria (Zheng et al. 2003), yeasts (Ulrich et al. 1995), or plants (Petruccelli et al. 2006). As for the applicability of those antibodies, they can be used in human and animal health, in diagnosis kits, and for organic synthesis.

7.2 The Antibody 14D9

The antibody 14D9 is an IgG₁-type murine antibody obtained by immunization against a piperidinium hapten. It is one of the fastest and most practical catalytic antibodies to date, being applicable for an enantioselective gram-scale synthesis (Reymond et al. 1991; Janghiri and Reymond 1994; Reymond et al. 1994; Zheng et al. 2004). 14D9, mechanistically related to enzymes as glycosidases, catalyses the highly enantioselective (>99 % ee) protonation of enol-ethers (Reymond 1999). It hydrolyzes a relatively broad spectrum of compounds with an aromatic nucleus, which is the recognition element. The best substrates for 14D9 are those with a stereochemistry (Z) in the double bond and an alquil substituent in the carbon to be protonated (Reymond et al 1993; Zheng et al. 2003).

As recombinant protein, 14D9 was expressed as a single-chain fragment (scFv), fused to the N utilization substance protein A (scFv-NusA), and as a chimeric fragment (Fab) in *E. coli* (Zheng et al. 2003). In *Nicotiana tabacum* plants 14D9 was expressed as the whole antibody (Petruccelli et al. 2006).

The potential use of 14D9 for releasing an essential growth factor (e.g.: biotin) from a specifically synthesized substrate is under study (Zheng et al. 2003).

7.2.1 14D9-Antibody Extraction and Analysis

For antibody extraction, samples are grinded using a cold mortar and pestle in cold PBS (0.24 g l⁻¹ KH₂PO₄, 1.44 g l⁻¹ Na₂HPO₄, 0.2 g l⁻¹ KCl, 8 g l⁻¹ NaCl, pH: 7.0–7.2) containing 10 µg ml⁻¹ leupeptin. The extracts are then centrifuged at 14,000 g for 20 min at 4 °C and the supernatant is separated to measure the antibody. Concentrations of antibodies possessing both heavy (γ) and light (κ) chains are evaluated by for γ and κ chains, a mouse IgG is used as a standard (Sigma Chemical Co). Only antibodies sandwich enzyme-linked immunosorbent assay (ELISA) using goat anti-mouse antibodies specific assembled into γ – κ chain complexes are detected. The functionality of the antibody is verified by competitive ELISA using bovine serum albumin (BSA) coupled to the 14D9 haptene (Petruccelli et al. 2006).

7.3 Establishment of Hairy Roots Expressing the Antibody 14D9

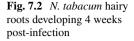
Transgenic tobacco expressing 14D9 were obtained by transformation with *Agrobacterium tumefaciens* LBA4404 (Petruccelli et al. 2006). Briefly, the gamma (γ) and kappa (κ) chains codifying for 14D9 were isolated from the mRNA of hybridoma cells and cloned into the binary plasmid pGA482. The 35S promoter of Cauliflower mosaic virus (CaM35S), the Tobacco-etch virus (TEV) leader signal, and the CaM35S terminator were also in the construct. A second version was designed, bearing the endoplasmic reticulum (ER) retention signal KDEL at the COOH terminal of the κ chain. The plasmids were introduced by electroporation in *Agrobacterium* spp. After stable transformation of tobacco, several strains expressing the chains γ , κ o κ -KDEL were obtained, a version expressing γ and κ chains (sec-Ab) and another expressing the γ and κ -KDEL chains (Ab-KDEL).

Seeds of both versions of recombinant plants, sec-Ab and Ab-KDEL, were germinated *in vitro*. Leaves and stems of plantlets were infected with *A. rhizogenes* LBA 9402 (Martinez et al. 2005). After 15 days of infection, roots tips emerged at the inoculation points (Fig. 7.1). The frequency of transformation was 98 % for the sec-Ab version and 87.5 % for the Ab-KDEL version. The nascent roots were transferred to Petri dishes with MSRT medium plus kanamycin (100 µg ml⁻¹) to eliminate *Agrobacterium* (Fig. 7.2). Transformation was confirmed by PCR. The hairy roots lines obtained (sec-Ab and Ab-KDEL) have different patterns of growth and 14D9 expression. The best producing lines of each version were selected and used in the following experiments. Wild type hairy roots were used as control.

After Agrobacterium was eliminated, hairy roots (sec-Ab, Ab-KDEL and wild type) were transferred to MSRT liquid medium without plant growth regulators (PGR) or antibiotics and maintained in culture by periodical transferences to identical fresh media (Alvarez et al. 1994). After 6 months in culture, hairy roots



Fig. 7.1 Hairy root tips appearing in the infection sites 15 days post-infection





were used to analyze growth and 14D9 production (Fig. 7.3). Hairy roots were transferred to a 2-bioreactor (Fig. 7.8), further experiments are being conducted in order to establish parameters of growth and 14D9 expression.

7.3.1 Kinetic of Growth and 14D9 Expression

Hairy roots of the sec-Ab, Ab-KDEL or wild type lines (% % W/V inoculum) were transferred to Erlenmeyer flasks containing MSRT culture medium. They were maintained at 24±2 °C, a 16-hs photoperiod given by fluorescent lamps (irradiance 1.8 w m⁻¹ s⁻¹) in a rotary shaker at 100 rpm during 25 days. Samples were taken by triplicate every five days. Cell growth (as DW) and 14D9 content (Martínez et al. 2005) were determined in each sample (Table 7.1). The specific growth rate showed significant differences (P<0.01) between the sec-Ab and Ab-KDEL lines respect to the wild type. The growth of wild type hairy roots was characterized by a continuous increase of biomass during the first 10 days followed by a 15 days-stationary phase. On the other hand, the exponential growth phase of the sec-Ab line extended up to the 20th day of culture, whereas in the case of the Ab-KDEL line the exponential phase continues up to the 25th day of culture (Fig. 7.4). Growth Index (GI) was higher for the Ab-KDEL line than for the sec-Ab line. The maximal biomass in the Ab-KDEL line was higher than in sec-Ab line. The antibody amount in the biomass in the sec-Ab line was lower than in the Ab-KDEL line, 14D9 was not detected in the culture medium (Martínez et al. 2005). The presence of the KDEL sequence increases the level of recombinant protein delivered into the secretory pathway, as happened with other recombinant proteins (Yoshida et al. 2004).



Fig. 7.3 N. tabacum hairy roots growing in MSRT culture medium without the addition of plant growth regulators

Table 7.1 Parameters of growth and 14D9 concentration in the biomass of *N. tabacum* wild type, sec-Ab and Ab-KDEL hairy root lines

N. tabacum line	μ (day ⁻¹)	GI	μ g14D9 mg FW ⁻¹
Wild type	$0.11 \pm 0.0.5$	0.98 ± 0.09	_
Sec-Ab	0.06 ± 0.01	1.03 ± 0.11	0.15 ± 0.01
Ab-KDEL	0.19±0.09	6.45±0.61	9.1±0.09

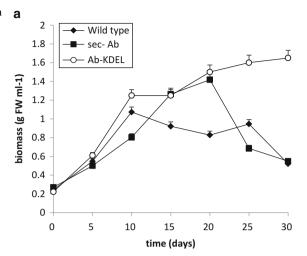
7.3.2 Influence of the Additives Dimethyl Sulfoxide (DMSO), Gelatine and Polyvinylpyrrolidone (PVP) on 14D9 Expression

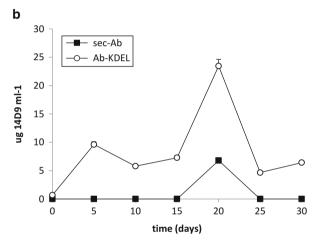
In order to increase 14D9 yields, the effect of dimethylsulfoxide (DMSO), gelatine and polyvinylpyrrolidone (PVP) was tested. Gelatine and PVP were selected for their activity as protein stabilizers, DMSO for the combined stabilizing and permeabilizing effect (Wongsamuth and Doran 1997).

7.3.2.1 Influence of Dimethylsulfoxide (DMSO)

An inoculum of 200 mg FW of hairy roots was transferred to 150 ml Erlenmeyer flasks containing 40 ml of MSRT medium without PGR. DMSO was added to the culture medium at different concentrations (2.8, 5.0, 8.0, and 10.0 % V/V) at the

Fig. 7.4 Profile of (a) growth of sec-Ab, Ab-KDEL and wild type *N. tabacum* hairy roots, and (b) 14D9 expression in sec-Ab and Ab-KDEL hairy root lines





14th day of culture (Fig. 7.5). DMSO had a deleterious effect on hairy roots growth at all the concentrations tested. As for 14D9 content, DMSO has a positive effect on the amount of 14D9 in the biomass of both transgenic lines (Fig. 7.6a), and on the protein total content (Fig. 7.6b) in the Ab-KDEL line. Those results could be a consequence of the permeabilising effect of DMSO facilitating the entry of nutrients in the cell (e.g.: aminoacids) to be used for protein synthesis (Whal et al. 1995). Also, it was postulated that DMSO could be acting as a chemical chaperone that stabilizes proteins in their native conformation with a protective effect against proteases (Brown et al. 1996).

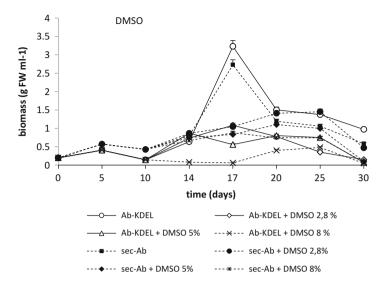


Fig. 7.5 Influence of the addition of DMSO at different concentrations (2.8 % V/V, 5 % V/V and 8 % V/V) on growth of N. tabacum sec-Ab and Ab-KDEL lines

7.3.2.2 Influence of Gelatine

Gelatine was added to the culture medium at three concentrations (1.0 g l⁻¹, 5.0 g l⁻¹, 9.0 g l⁻¹) at the 22nd day of culture corresponding to the highest 14D9 accumulation in non-treated hairy roots. At a concentration of 5.0 g l⁻¹ gelatine had a positive effect on 14D9 concentration in the culture medium. However, it had a negative effect on growth at concentrations higher than 1.0 g l⁻¹. The maximal concentration of 14D9 in the culture medium corresponded to a concentration of gelatine of 5.0 g l⁻¹, with a 14D9 concentration of 15 µg 14D9 ml⁻¹ at the 22nd day of culture. As for the %TSP in the biomass it does not show significant differences between the treatments and the control (Fig. 7.7). The positive effect of 5.0 g l⁻¹ gelatine on the amount of the antibody concentration in the culture medium could be attributed to a blocking of specific interactions between the antibody and the Erlenmeyer glass surface, a competition with the substrate for the enzymes that degrades the immunoglobulin, modification of interactions among the recombinant IgG and components of the MSRT culture medium (Martínez et al. 2005, Doran 2006). The obtained results agree with those reported by Wongsamuth and Doran (1997) which demonstrated a stabilizing effect of gelatine, at concentrations of 1.0-9.0 g l⁻¹, on the heavy chain of the monoclonal antibody Guy's 13 in N. tabacum suspension cell cultures.

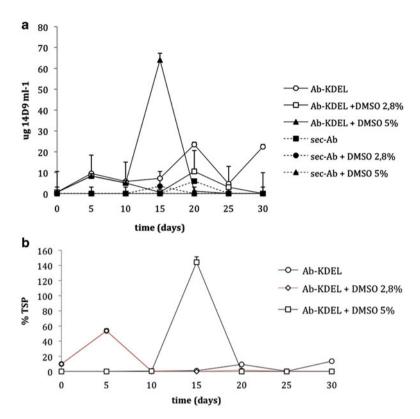


Fig. 7.6 The 14D9 content in the biomass of sec-Ab and Ab-KDEL *N. tabacum* hairy root lines, and **(b)** the total soluble protein content (%TSP) in the biomass of the Ab-KDEL *N. tabacum* hairy root line

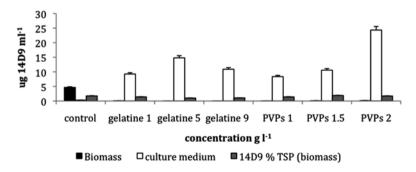


Fig. 7.7 Influence of gelatine (1 g l^{-1} , 5 g l^{-1} , 9 g l^{-1}) and PVP (1 g l^{-1} , 1.5 g l^{-1} , 2 g l^{-1}) on 14D9 amount in the biomass, the culture medium and on the 14D9 % TSP in the biomass



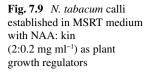
Fig. 7.8 *N. tabacum* hairy roots, line sec-Ab growing in a 2 l- bioreactor (Minifors) in MSRT media without plant growth regulators

7.3.2.3 Influence of Polyvinylpyrrolidone

Polyvinylpyrrolidone (PVP) is a versatile polymer, water soluble, with excellent colloidal, stabilizing and complexing properties, being at the same time metabolic and physiological inert (Magnuson et al. 1996). For analyzing its effect on 14D9 production, PVP was added to the Ab-KDEL hairy root cultures at three different concentrations (1 g l⁻¹, 1.5 g l⁻¹ and 2.0 g l⁻¹). The effect was analyzed at the 22nd day of culture that corresponds to the highest 14D9 amount in the hairy roots without treatment. The addition of PVP at a concentration of 1.0 gl⁻¹ had significant positive effect (P<0.01) on growth in the Ab-KDEL line (Fig. 7.7). Other researchers have reported a negative effect on growth of PVP concentrations higher than 3.0 g l⁻¹ (Magnuson et al. 1996). On the other hand, 14D9 concentration increased significantly (P<0.01) in the culture medium (24 μ g ml⁻¹) at a PVP concentration of 2.0 g l⁻¹ (Martínez et al. 2005). Maybe the protective effect of PVP avoids the antibody denaturalization or its adherence to the contact surfaces (Doran 2006) (Fig. 7.8).

7.4 Production of 14D9 in Cell Suspension Cultures

From a biotechnological point of view it is desirable to perform a productive process in suspended cells for the more straight control of the environmental conditions at cellular level. We have established cell suspension cultures of both 14D9 expressing-recombinant lines (sec-Ab and Ab-KDEL).





7.4.1 Establishment of Calli Cultures

Pieces of leafs of transgenic plants expressing the antibody 14D9 in both versions (sec-Ab and Ab-KDEL) were transferred to Petri dishes containing MSRT solid medium (8 g l⁻¹ agar, 30 g l⁻¹ sucrose) with the addition of one of NAA: kinetin (2 mg l⁻¹: kinetin 0.2 mg l⁻¹). The cultures were kept in a chamber at 24±2 °C, and a 16-hs photoperiod given by fluorescent lamps (irradiance 1.8 w m⁻¹ seg⁻¹). After a couple of weeks, calli appeared in the wounded surfaces. They were separated, transferred to fresh media, and subcultured monthly (Fig. 7.9). At each subculture, samples were taken by triplicate to measure 14D9. Using this methodology, the more productive and stable lines are maintained since 2005.

7.4.2 Establishment of Cell Suspension Cultures

Friable calli from the lines sec-Ab and Ab-KDEL were transferred to Erlenmeyer flasks (5 % W/V) with MSRT liquid medium plus sucrose (30 g l⁻¹) and NAA: kinetin (2 mg l⁻¹: 0.2 mg l⁻¹). The suspended cells (Fig. 7.10) were transferred to identical fresh media (maintenance medium) every 20 days, and maintained at 24 ± 2 °C, a 16-hs photoperiod (irradiance 1.8 w m⁻¹ seg⁻¹) in an orbital shaker at 100 rpm (López et al. 2010).

Fig. 7.10 *N. tabacum* cell suspension culture, line Ab-KDEL



7.4.3 Kinetic of Growth and 14D9 Expression in N. tabacum Cell Suspension Lines sec-Ab and Ab-KDEL

For analyzing the profile of growth and 14D9 production of cell suspension cultures, 2.0 g FW of an 8-day-old culture were transferred to 150 ml-Erlenmeyer flasks with 40 ml of MSRT maintenance medium and cultured in the same conditions described in Sect. 7.4.2 during 30 days. Samples were taken every 5 days for determining cell growth and to quantify 14D9.

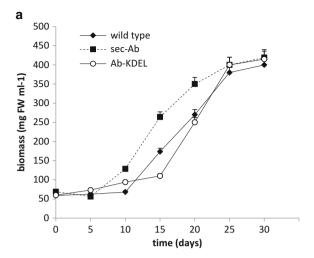
The specific growth rate and the amount of 14D9 in the biomass were significant higher in the Ab-KDEL line than in the sec-Ab and wild type lines. However, there are no significant differences in maximal biomass among the lines (Fig. 7.11, Table 7.2).

7.4.4 Influence of DMSO

DMSO was used in an attempt to increase the amount of 14D9 in the culture medium because it was reported that it can produce a stabilizing effect on proteins by forming hydrogen bonds with the protein proton donor groups (Henderson et al. 1975) acting as a chemical chaperone (Welch and Brown 1996).

To express 14D9, DMSO was added at the 3rd day of *N. tabacum* lines sec-Ab and Ab-KDEL cultures, at different concentrations (1.5, 2.0, 2.5 %). At all the concentrations tested DMSO has a negative effect (P<0.05) on growth. At a 1.5 % concentration DMSO produced an 8-fold increase of 14D9 in the culture medium at

Fig. 7.11 (a) Kinetic of growth of *N. tabacum* wild type, sec-Ab and Ab-KDEL cell suspension cultures, (b) 14D9 accumulation in the biomass of both transgenic lines



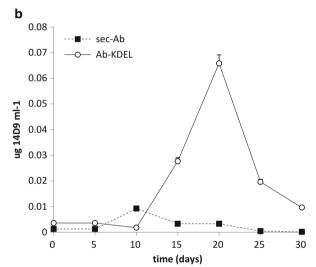


Table 7.2 Parameters of growth and 14D9 production on N. tabacum wild type, sec-Ab and Ab-KDEL lines

N. tabacum line	μ (day ⁻¹)	td	Maximal biomass (mg ml ⁻¹ FW)	14D9 (μg 14D9 g ⁻¹ FW)
Wild type	0.086	8.05	400	_
sec-Ab	0.069	10.7	419	0.012
Ab-KDEL	0.149	4.62	415	0.470

the 10th day of culture in the line sec-Ab, while at a 2.0 % concentration there is a 5-fold increase in the culture medium at the 11st day of culture in the line Ab-KDEL. Total protein and 14D9 content in the biomass did not increase.

7.4.5 Effect of Gelatine and PVP on Growth and 14D9 Yield

Protein stabilizing agents and protease inhibitors are employed to increase the amount of recombinant proteins in cultures. Some of the protein stabilizers used are gelatine, bovine seroalbumin (BSA) (for protein-based stabilization), mannitol (to regulate the osmotic pressure of the medium to minimize cell lysis), PEG and other polymers (as stabilizing agents and to protect proteins from plant cell denaturing agents) (Benchabane et al. 2008; Guillon et al. 2006; Magnuson et al. 1996; Sharp and Doran 2001).

Different concentrations of gelatine (1.0, 5.0 or 9.0 g l⁻¹) or PVP (1.0, 1.5 or 2.0 g l⁻¹) were added to the culture medium at the first day of culture. Samples were taken by triplicate at the 22nd day of culture to measure FW, DW, and antibody accumulation in the biomass and in the culture media. The culture conditions were also the same as described above. When PVP was added at 1.0 g l⁻¹ and 1.5 g l⁻¹ concentration, the antibody in the biomass increased from 1.4 % TSP to 4.8 % TSP and 2.99 % TSP respectively in Ab-KDEL line. In the case of the sec-Ab line the 14D9 yield increased from 0.17 % TSP to 1.16 % TSP with a PVP concentration of 1.5 g l⁻¹ (Fig. 7.12).

As for the amount of antibody in the culture medium, an increase from 0.06 %TSP (control) to 0.18 %TSP and 0.15 % TSP was obtained with 1.0 and 1.5 g l^{-1}

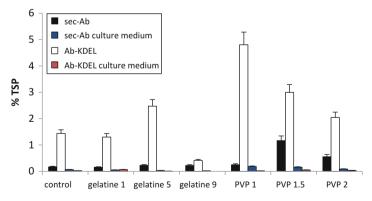


Fig. 7.12 Effect of gelatine $(1, 5 \text{ and } 9 \text{ g l}^{-1})$ and PVP $(1, 1.5 \text{ and } 2 \text{ g l}^{-1})$ on 14D9 accumulation (as % of total soluble protein) in the biomass and in the culture medium of *N. tabacum* sec-Ab and Ab-KDEL transgenic lines

PVP respectively for sec-Ab cell suspension cultures; no significant changes were detected in the culture media of the Ab-KDEL cell suspension line. Concerning the influence of gelatine, at a concentration of 5.0 g l⁻¹ the antibody yield increased from 1.43 % TSP to 2.47 % TSP in Ab-KDEL cell suspensions. No significant influence of levels in the biomass of the sec-Ab line, or in the culture medium was determined (López et al. 2010).

The beneficial effect of PVP is attributed to its excellent complexing, stabilizing and colloidal properties, while it is metabolically and physiologically inert, or for being taken as sacrificial substrate for protease activity. Moreover, PVP would be the preferred additive in a production process for being a non-human and non-animal source.

Protease concentration in the biomass was 1.0 U g FW⁻¹ h⁻¹, and remains constant along the culture, whereas in the media the protease activity increased after the 10th day in culture to a maximal level of 0.16 U g FW⁻¹ h⁻¹ until the end of the culture.

Our results are partially in agreement with those reported for other authors (Sharp and Doran 2001; Wongsamuth and Doran 1997) when expressing the secreted version of the monoclonal antibody Guy's13 in *N. tabacum* cell suspensions and hairy roots. They did not found a significant influence of PVP on antibody accumulation in the biomass of cell suspensions and have established that PVP and gelatine diminishes antibody content in hairy root biomass. However, they have reported an increase of total antibody accumulation both in cell suspension as in hairy roots when PVP or gelatine were added at a concentration of 1.5 g l⁻¹ or 9.0 g l⁻¹ respectively due to an increase in antibody accumulation in the culture medium (López et al. 2007).

7.4.6 Kinetic of Growth and 14D9 Expression After Three Years in Culture of the sec-Ab and Ab-KDEL Lines

After three years in culture the profile of growth and 14D9 production in the sec-Ab and Ab-KDEL lines was studied and compared to those of the first year in culture. As is shown in Fig. 7.13, a reduction of the lag phase from 10 to 3 days is evident. Also the specific growth rate (μ), and the amount of 14D9 in the biomass increased (Table 7.3). No significant differences (P>0.05) were found in the final biomass among the transgenic and the wild type lines demonstrating that the expression of the heterologous protein do not has a negative consequence on cell growth (López et al. 2010).

The amount of sucrose in the culture medium was 11.4 g l^{-1} in the wild type at the end of the culture, while for the sec-Ab and Ab-KDEL lines, sucrose was totally consumed at the 10th day and at the 28th day of culture respectively. The maximal biomass yield related to the consumed substrate (Yx/s) was in all cases into the average values for plant cells $(0.3-0.7 \text{ g DW g sugar}^{-1})$ (Payne et al. 1991).

Fig. 7.13 (a) Kinetic of growth of *N. tabacum* wild type, sec-Ab and Ab-KDEL lines and (b) 14D9 amount in the biomass of the transgenic lines after 3 years in culture

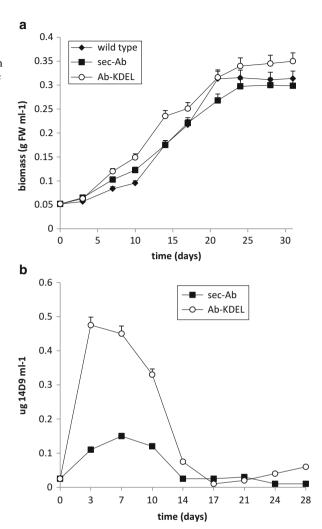


Table 7.3 Parameters of growth and 14D9 production in *N. tabacum* wild type, sec-Ab and Ab-KDEL lines after 3 years in culture

Line	μ (day ⁻¹)	td (days)	GI	Final biomass (g FW)	Yx/s (g DW g consumed sucrose ⁻¹)	μg 14D9 g FW ⁻¹
Wild type	0.098	7.07	6.65	13.73 ± 1.30	0.711±0.123	_
Sec-Ab	0.086	8.06	5.88	12.20 ± 1.20	0.419 ± 0.011	0.73 ± 0.05
Ab-KDEL	0.123	5.64	7.13	14.79 ± 2.53	0.467 ± 0.049	8.21 ± 0.82

There is a threefold increase of 14D9 level in the Ab-KDEL line respect to the sec-Ab line, and a twofold increase respect to leaves of the whole transformed plant (Petruccelli et al. 2006). The differences in 14D9 levels between the sec-Ab and Ab-KDEL line confirmed the protector effect of the ER-retention on antibody accumulation. The more oxidant environment, with less proteases and high amount of chaperones like BiP, promotes the correct folding and decrease the antibody degradation (Schouten et al. 1997). The fall in 14D9 amount at the end of the cultures in both transgenic lines can be attributed to a diminution in the transgene expression (RNAm), by an increase in the activity of proteases not detected by the test of azocaseine digestion, and by the formation of 14D9 aggregates that can produce false negatives (Sharp and Doran 2001; Schouten et al. 1996).

7.5 Influence of Mannitol on Growth and 14D9 Expression

Mannitol produces an osmotic stress in plant cells that alter their gene expression and increase the proteins synthesis (Soderquist and Lee 2005). Also, it was described a certain stabilizing effect on proteins (Wimmer et al. 1997). We analyzed the effect of mannitol (90 g l⁻¹) on cell growth and 14D9 yield in *N. tabacum* suspended cells (Fig. 7.8). Fresh weight and μ decreased significantly (P<0.05) both in the sec-Ab and Ab-KDEL, an effect derived from the high osmolality of the culture medium (López et al. 2010). That negative effect of the osmotic stress on cell growth was also reported for hybridomes and animal cultures, and in *N. tabacum* suspended cells expressing an IgG in the presence of 17 g l⁻¹ mannitol (Tsoi and Doran 2002).

The utilization of sucrose was also affected. The three lines (sec-Ab, Ab-KDEL, wild type) consumed sucrose during growth. Sucrose is hydrolyzed to glucose and fructose by the activity of invertases associated to the plant cell walls; those sugars are used as carbon source by plant cells. Glucose accumulated at the beginning of the culture when sucrose was abundant and the hydrolysis of sucrose and glucose production was higher than the glucose consumed by plant cells. When sucrose decreased in the culture medium, the glucose concentration remained constant because the rate of production and consumption are balanced, finally glucose concentration decreased when the sucrose in the culture medium is almost zero. In the presence of an osmolite as mannitol the consumption of sucrose is lower; perhaps mannitol can be a supplementary carbon source, as happen in suspension cell cultures of celery that use mannitol as carbon source (Table 7.4).

Table 7.4 Influence of mannitol (90 g l^{-1}) on specific growth rate (μ), growth (final biomass) and antibody content

N. tabacum line	μ (day ⁻¹)	Final biomass (g l ⁻¹)	14D9 (μg ml ⁻¹)
Sec-Ab	0.086 ± 0.002	12.20±1.20	0.018±0.006
Sec-Ab+mannitol	0.052 ± 0.006	9.42±0.79	1.96±0.20
Ab-KDEL	0.123 ± 0.0053	14.79 ± 2.53	0.20 ± 0.082
Ab-KDEL+mannitol	0.11 ± 0.030	13.00±1.25	2.31±0.18

Total protein content and 14D9 increased in the biomass (P < 0.05) but not in the culture medium (P > 0.05). In the biomass the values were twofold higher respect to the control without significant differences between the transgenic lines.

The level of antibody in the culture media was not affected by the presence of mannitol, discarding the stabilizing effect of mannitol on proteins. The antibody secreted to the culture medium was 0.20 % of the amount in the biomass for the sec-Ab line and 0.02 % of the amount in the biomass for the Ab-KDEL line. In the sec-Ab line, 14D9 would be retained in the apoplast, the space between the cell membrane cell wall. The exclusion size of the cell wall pores is approximately 20-30 kDa (Carpita et al. 1979) although, in some cases proteins of 50 kDa, and even whole antibodies of 150 kDa, can pass through the cell wall (Hein et al. 1991). In our experiments 14D9 is apparently retained in the apoplast (sec-Ab) or in the ER (Ab-KDEL). The low levels of 14D9 in the culture medium can be a consequence of an inefficient retention in the ER that permit an antibody escape to the apoplast (Petruccelli et al. 2006), or to cell lysis and the consequent liberation of the antibody to the culture medium. The loss of 14D9 in the culture medium at the end of the culture can be attributed to its adsorption to the vessel walls (Doran 2006), to the degradation by proteases, which were detected at lower activities than in the biomass, or to a combination of both phenomena. The direct ELISA demonstrated the ability of the recombinant 14D9 of recognizing and binding its haptene.

7.6 Large-Scale Production in a 2-l Bioreactor

Suspended cells of the Ab-KDEL line (inoculum size 1 % or 5 %, by W/V) were transferred to a 2-1 stirred-tank bioreactor (Minifors, Infors HT®, Switzerland) containing 1.01 of MSRT medium with NAA: kinetin (20:02 mg l⁻¹) as PGR (Fig. 7.14). A marine propeller produced the mechanical agitation and a porous metal sparger provided the bubble aeration. Culture conditions were 100 rpm, 0.1 vvm, and 24±2 °C. Relative partial O2 pressure and pH were monitored on-line. Samples were taken every 2 days during a culture period of 15 days, for measuring FW, DW, and 14D9 concentration. Three replicates were used in all analytical determinations. Analysis of variance (ANOVA) was performed for each test. Table 7.5 shows the parameters of growth and antibody content of *N. tabacum* in the 2-l bioreactor.

Regarding the GI and the antibody content, both were higher with a 1 % P/V than with a 5 % P/V inoculum size. As for biomass yield respect to the carbon source (YX/S), it was significant lower in the bioreactor when the inoculum size was 5 % V/V respect to the inoculum size of 1 % V/V probably due to a nutrient limitation derived from the highest cell density in the culture (Marconi and Alvarez 2014b).

Comparing the process performed in Erlenmeyer flasks and the bioreactor, the antibody yield was significantly higher in the 2-l bioreactor than in Erlenmeyer flasks. Those results are predictable considering the highest availability of nutrients and the earlier antibody peak production attained in the bioreactor (between the

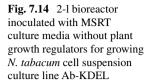




Table 7.5 Parameters of growth and 14D9 production of *N. tabacum* Ab-KDEL line in a 2-1 Minifors bioreactor at two inoculum sizes (1 % P/V and 5 % P/V)

Inoculum size (% P/V)	μ (day ⁻¹)	Final biomass (mg FW ml ⁻¹)	14D9 (μg g FW ⁻¹)
1	0.084	70.9	0.66
5	0.291	177.91	0.21

days 5 to 10 of culture) than in Erlenmeyer flasks (between the days 10 to 20 of culture). Comparing the performance of the Ab-KDEL cell suspension culture in the bioreactor with that of hairy roots in Erlenmeyer flaks, yield expressed as % TSP was also higher in suspended cells growing in the bioreactor. However, the productivity values were considerable lower than those of hairy roots that would be attributable to the fast growth and high productive biomass characteristics of hairy root cultures.

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7.7 Conclusive Remarks

The 14D9 catalytic antibody was expressed in *N. tabacum* hairy roots and undifferentiated *in vitro* cultures. Figure 7.15 summarizes the procedures followed to optimize yields. Both systems (hairy roots and cell suspension cultures) were a feasible antibody productive platform. The presence of the KDEL ERretention signal and the use of PVP at a 1 % g l⁻¹ concentration resulted in the highest antibody yields in Erlenmeyer flasks. The scale up of Ab-KDEL suspended cells to a 2-l stirred-tank bioreactor increased 14D9 yield (expressed as % TSP) but productivity remained higher in hairy root cultures due to their highest productive biomass.

Comparing 14D9 yields obtained in all the platforms and systems tested, we can conclude that hairy roots growing in Erlenmeyer flasks and Ab-KDEL cell suspension cultures growing in a 2-l bioreactor gave the highest 14D9 yields. Further work is being conducted in order to optimize 14D9 production by *N. tabacum* cell suspension and hairy root cultures in a bioreactor.

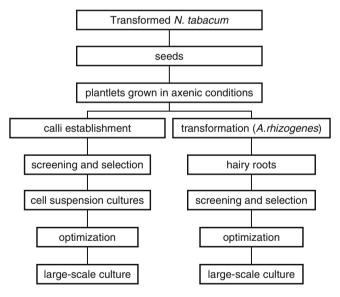


Fig. 7.15 General procedure followed to establish *N. tabacum in vitro* cultures for producing 14D9

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Chapter 8 Expression of the Potentially Immunogenic Truncated Glycoprotein E2 (From Viral Bovine Diarrhoea Virus) in Nicotiana tabacum

Abstract Viral Bovine Diarrhoea (VBD) is a contagious infection disease caused by the viral bovine diarrhoea virus (BVDV) producing high economic losses for its effects in the respiratory and reproductive system. Besides bovines, BVDV also affects sheep, goats, and wild ruminants, which are potential reservoirs of the virus.

The main purpose of a program for controlling BVDV should be the prevention of the foetal infections, avoiding the birth of persistently infected animals (PIA), and preventing acute infections. Those goals can be achieved preventing the exposure to the virus by removing the PIA from the herd, and by increasing the immunity to BVDV through vaccination.

The glycoprotein E2, as the principal immunogen of the BVDV, is the main target for neutralizing antibodies. In the last decade, studies were performed to develop vaccines with a recombinant E2 of prokaryotic and eukaryotic origin. E2 was expressed in *E. coli*, mammal's cells through the vaccinia system, insect cells and plants. In insect cells and plants the E2 expressed was able to induce specific neutralizing antibodies being potential production platforms for the development of a new generation of vaccines.

Keywords Viral bovine diarrhoea • Glycoprotein E2-molecular farming • *Nicotiana tabacum*-plant transformation • Plant-made proteins

8.1 Introduction

Vaccines are fundamental tool to fight the majority of infectious diseases; therefore, the recent outbreaks have triggered huge efforts to R&D of new vaccines. The limiting steps are the considerable extent of production processes, high costs, and the need of a fast response (Alvarez 2012). Besides the traditional production methods, protein immunogens to produce subunit vaccines are being produced in yeasts, insect cells, plant cell cultures and transgenic plants with different degree of success (Bolin and Ridpath 1996; Smith et al. 2011; Xu et al. 2012; Hefferon 2013).

The Bovine Viral Disease produces considerable economical losses when outbreaks in cattle, which put in focus the research for new generation vaccines.

8.2 Viral Bovine Diarrhoea

Viral Bovine Diarrhoea (VBD) is a contagious infection disease caused by the viral bovine diarrhoea virus (BVDV), a virus of the genus Pestivirus (family Flaviviridae). BVDV affects bovines, causing high economic losses for its activity in the respiratory and reproductive system (Lértora 2003). Besides, BVDV affects sheep, goats and wild ruminants, which are potential reservoirs of the virus (Bracamonte et al. 2006). The virus was described for the first time in 1946 in the United States of America, soon after it was detected in many countries as England, Australia, Kenya, Germany and Argentina.

8.3 The Viral Bovine Diarrhoea Virus (BVDV)

The BVDV is a positive chain RNA virus, antigenically related to other Pestivirus as the Classic Swine Fever Virus (CSFV) and the ovine Border Disease Virus (BDV) (Pringle 1999). Besides the antigenic variation, the isolates of BVDV can be classified in cytopathic (cp) and non-cytopathic (ncp) strains according to their ability to induce cytopathic effects in cell cultures. Several BVDV strains maintain their cytopathogenicity in a broad spectrum of host tissues, while others change during the passages through different host cell systems.

8.4 Vaccines

The main purpose of a program for controlling BVDV should be the prevention of the foetal infections, avoiding the birth of persistently infected animals (PIA), and preventing acute infections (Harkness 1987). Those goals can be achieved preventing the exposure to the virus by removing the PIA from the herd, and by increasing the immunity to BVDV through vaccination.

The vaccines currently in the market do not produce a significant reduction of BVDV prevalence, which drives research of more effective and secure vaccines. There are two types of commercial vaccines: modified-live vaccines (MLV) and inactivated vaccines (IV) (Bolin and Ridpath 1995). In general, in both cases, the neutralizing titres are in the order of 1:2,000 (Fulton and Burge 2001).

Although it was demonstrated that passively acquired antibodies could protect against the challenge with BVDV (Bolin and Ridpath 1995), the relationship between the neutralizing titre and the protective effect it is not yet clear (van Oirschot et al. 1999). However, the study of the efficacy of vaccines after vaccination lies in the sero-conversion test and other measurable parameters, as rectal temperature and leucopoenia, after a viral challenge in vaccinated animals.

BVDV also suppresses the immune system facilitating other pathogens entry. Consequently, a multi-vaccine complex with other antigens as herpes bovine-1

virus, parainfluenza-3 virus, respiratory syncytial virus, and different species of *Pasteurella* and *Haemophilius*, is commonly intramuscular or subcutaneously administered (van Oirschot et al. 1999).

8.5 Role of the Adjuvant

Adjuvants, which increase the response to antigens, are vaccine components that contribute to the delivery of the immunogen and to the maintenance and modulation of the immune response (Aucouturier et al. 2001). Besides, as they improve the vaccine efficacy, they reduce the amount of antigen required in the formulation. Liveviral traditional vaccines do not require the addition of an adjuvant. The modern recombinant vaccines, with highly purified synthetic antigens, need adjuvants for inducing the long-term protective immune response. Aluminium salts are the most employed adjuvants in human vaccines, but they are weak and promote mainly the induction of neutralizing antibodies than cellular immunity. Other adjuvants in use are oily emulsions, bacterial products (B subunit of the Vibrio colerae toxin), viral products (virus-like particles), plant secondary metabolites (saponins), biodegradable particles (liposome), etc. (Lambrecht et al. 2009; Reed et al. 2008; Aucouturier et al. 2001). Adjuvants may produce their effects through different mechanisms, recruiting innate immunity as a consequence of its deposit in the tissues, which results in a slow release of antigens from the injection site. Or, by maintenance of the antigen appropriate conformation through specific targeting mechanisms. Adjuvants should be chosen to optimise the required response with minimal side effects (WHO guidelines 2013; O'Hagan and Derek 2007).

8.6 The Glycoprotein E2

8.6.1 Antigenic Structure of the Glycoprotein E2

The BVDV glycoprotein E2 is the most important inductor of neutralizing antibodies (Donis et al. 1988; Magar et al. 1988; Weiland et al. 1999; Wensvoort and Terpstra 1988). The precise localization of its antigenic determinants and the relationship among them are not completely known. Some researchers have described possible epitope localization based on the reactivity patterns with monoclonal antibodies (Toth et al. 1999; Paton et al. 1992; Xue et al. 1990; Moennig et al. 1989; Corapi et al. 1988; Bolin et al. 1988). Not all the antigenic sites contribute to the neutralization of antibodies, but several BVDV-1 strains share an immunodominant neutralizing antigenic domain to which most of the neutralizing monoclonal antibodies bind (Paton et al. 1992). That domain is composed of several epitopes that map to the N-terminal region, whose conformation is probably defined by discontinuous aminoacid sequences. Those epitopes were also described for CSFV

(Yu et al. 1994; van Rijn et al. 1993). Two other epitopes were localized, one that is a fragment containing the last 90 aminoacids of the C- terminal end and a discontinuous epitope whose formation would depend on the expression of the whole protein (Toth et al. 1999). At least another lineal epitope was reported (Deregt et al. 1998a; Yu et al. 1996).

Differently from BVDV-1 where the conserved neutralizing epitopes map in a dominant immunodomains, in BVDV-2 the neutralizing antibodies bind to highly conserved epitopes in three antigenic domains (Deregt et al. 1998b). On the other hand, Ciulli et al. (2009) have reported the presence of an antigenic site in a population of viral variants with a low degree of antigenicity that could avoid the host immune system.

E2 forms homodimers and heterodimers by means of disulfide bonds with E1 (Branza-Nichita et al. 2001; Durantel et al. 2001; Thiel et al. 1991; Weiland et al. 1999) and remains associated to the Golgi membranes (Greiser-Wilke et al. 1991; Grummer et al. 2001; Weiland et al. 1999). Analysis of the crystal structure of E2 has revealed unique protein architecture with three domains (I, II and III), two Ig-like domains followed by an extended β - stranded domain with other fold. An essential role of His762 in pH sensing was proposed. Two Antigenic domains were mapped in domain I, two in domain II, and none in domain III suggesting that the latter is not exposed on the viral surface. One face of E2 appears to be solvent exposed while the opposite one is probable in the interface with E1 (Li et al. 2013). On the other hand, the absence of a class II fusion protein fold in E2, and the disorder of the N-terminal domain at low pH were reported (El Omari et al. 2013).

8.6.2 The BVDV Recombinant E2 Glycoprotein as Immunogen in Alternative Production Platforms

The glycoprotein E2, as the principal immunogen of the BVDV, is the main target for neutralizing antibodies. In the last decade, studies were performed to develop vaccines with a recombinant E2 of prokaryotic and eukaryotic origin.

The E2 expressed in bacteria did not induce neutralizing antibodies in rabbits. As the majority of the E2 neutralizing epitopes is discontinuous E2 folding in prokaryotes is inaccurate, which demonstrate that a correct conformation of E2 is fundamental for inducing a neutralizing immune response (Yu et al. 1994). The expression of E2 in mammal cells by a recombinant Vaccinia system induced low neutralizing antibody titres in rabbits and bovines (Tijssen et al. 1996).

The E2 protein with the precedent hydrophobic sequence (corresponding to the C- terminal region of the E1 protein) and without its membrane-anchoring region (last 31 aminoacids) expressed in insect cells produced neutralizing antibodies in bovines and rabbits (Bolin and Ridpath 1996; Tijssen et al. 1996). The reported yields were $10 \, \mu g \, E2 \, ml^{-1}$ in insect cell lysates infected with recombinant baculovirus (Grigera et al. 2006; Marzocca et al. 2007), and $1-2 \, \mu g \, E2 \, ml^{-1}$ in *Escherichia coli* (Toth et al. 1999).

The E2 protein has also been expressed in mammal recombinant viral systems (HEK293T cells) (Donofrio et al. 2006) and has been used as attenuated experimental vaccines (Baxi et al. 2000; Elahi et al. 1999; Kweon et al. 1999).

A chimeral recombinant E2 protein (rE2) was expressed in the transient system Vaccinia and baculovirus (Reed et al. 1999; Grigera et al. 2000; Marzocca 2003). The rE2 has demonstrated identical characteristics to its wild viral chimeral counterpart in terms of its ability to react with antibodies depending in conformation, glycosylation capacity and capacity to form dimmers. Also, rE2 resulted in a potent immunogen in mice, rabbits and bovines being able to induce an anti-BVDV response compatible with the protection of bovines.

Promising results were obtained by the expression of a recombinant glycoprotein E2 in plants (Nelson et al. 2012; Aguirreburualde et al. 2013).

8.7 Plant Systems for Producing Vaccines

The use of plants as a vaccine production platform requires a careful selection of the antigens to be expressed and the development of constructs for a high-level expression of antigens in the plant tissue (Tiwari et al. 2009). Table 8.1 show a brief list of immunogenic antigens expressed in plants. Some of them have demonstrated its preventive and therapeutic value and are in clinical evaluation (Arntzen et al. 2005; Koprowski 2005; Ma et al. 2005; Desgranges 2004; Mason et al. 2002). The classical example is CaroX ® against *Streptococcus mutans* to prevent dental caries (Gavilondo and Larrick 2000; Larrick and Thomas 2001).

Disease	Antigen	Species	Reference
Rinderpest	Hemaglutinine	Arachis hypogaea	Kandelwal et al. (2004)
Foot and mouth disease	VP1	Arabidopsis thaliana,	Dus Santos and
	P1-2A/3C	Medicago sativa, Solanum tuberosum	Wigdorovitz (2005)
Classic Swine Fever	E2	Medicago sativa	Legocki et al. (2005)
Rotavirus	VP6	N. tabacum	Dong et al. (2005)
Toxoplasmosis	SAG1	N. tabacum	Laguía-Becher et al. (2010)
Malaria	Pfs25	N. benthamiana	Farrance et al. (2011)

Table 8.1 Some examples of immunogenic antigen produced in plants

8.8 Expression of the Glycoprotein E2 in N. tabacum

The immunogenicity of the recombinant E2 glycoprotein (rE2) expressed in tobacco and its potential use as immunogen in an alternative vaccine was reported (Nelson et al. 2012). Besides the gene for the E2 glycoprotein without its transmembrane domain, the construct carried the signal sequence of the 2S2 seed storage protein of *Arabidopsis thaliana* that drives the protein to the secretory pathway, the KDEL ER–retention signal, and a hexa-histidine tag (His-tag) placed before the KDEL to facilitate protein purification. The derived plasmid pK-2S2-tE2-His-KDEL was introduced in *A. tumefaciens* by electroporation and the resultant *Agrobacterium* was infiltrated in *N. tabacum* leaves of 2-day old plants as was described in (Nelson et al. 2012) The maximum tE2 expression level was attained at the 4th day post-infection. SDS-Page and non-reducing Western blot showed the expression of an E2 dimmer of approximately 80 kDa, like the positive control (Fig. 8.1). The reducing Western blot showed a band of 35 kDa, corresponding to the tE2 monomer.

The expression level was of approximately 20 μg E2 per gram of infected leaf (1.3 % TSP) (Fig. 8.2).

8.8.1 Induction of Specific Neutralizing Antibodies

To analyse the ability of the recombinant E2 expressed in *N. tabacum* to induce specific neutralizing antibodies two different vaccine formulations were tested in guinea pigs. Guinea pigs could replace bovines when testing the immunogenicity of commercial or experimental BVDV vaccines for the optimal correlation between bovine-guinea pig models (Fernández et al. 2009; Jordão et al. 2011). The formulations tested were made with the crude plant extract containing 20 μg ml⁻¹ of

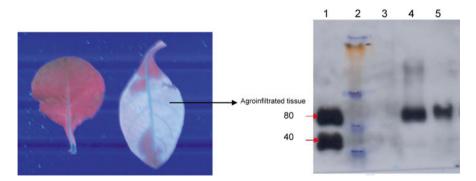
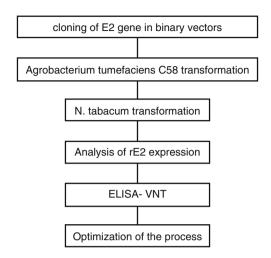


Fig. 8.1 (a) *Left*: leaf of *N. tabacum* without treatment, *right*: leaf of agroinfiltrated *N. tabacum* (b) Western blot

Fig. 8.2 General scheme of the strategy employed for analysing the expression of the recombinant E2 glicoprotein of BVDV in *N. tabacum* and its ability to induce specific neutralizing antibodies



recombinant E2 in a ratio 40:60 with and aqueous adjuvant (Al(OH)3 Hydrogel®) and in a ratio 90:10 with an oily adjuvant (Montanide ISA70 SEPPIC®). Blood samples were taken at time 0 and 15 and 30 days after vaccination. The presence of specific anti-E2 antibodies in blood of vaccinated animals were detected by ELISA and a virus neutralization test (VNT). Values higher than 0.6 corresponding units (OD $_{405}$ or VNT titre) were considered positive.

8.8.2 Evaluation of Anti-E2 Specific Antibodies by ELISA

The titre of the serum was calculated as the reciprocal of the dilution in which OD corresponds to twice the value of the OD of the negative control. Seroconversion was detected in 86 % of animals with the formulation plant extract: oily adjuvant, while it was 75 % with the aqueous adjuvant (Nelson et al. 2012).

8.8.3 Virus Neutralization Test (VNT)

The OIE (2004) recommended the VNT, defined as the loss of infectivity through reaction of the virus with specific antibody, to detect sera neutralizing antibodies (Reed and Muench 1938). The results obtained showed that with the formulation containing the oily adjuvant three out of seven animals produced neutralization antibodies, and that all the animals showed neutralizing antibodies with the aqueous adjuvant. Sham vaccines did not induce neutralizing antibodies (Nelson et al. 2012).

8.9 Conclusive Remarks

Several difficulties arise from the use of the some of the vaccines against VBDV actually in use. Those difficulties are mainly related to the occurrence of secondary effects such as immunosuppression and congenital defects, the emergence of persistent infections by non-cytopathic BVDV biotypes, the in utero infections and/or immunosuppression produced by modified live vaccines, and the introduction of contaminant pathogens by modified-live, attenuated or inactivated vaccines produced in bovine cell cultures (Erickson et al. 1991; Nobiro et al. 2001).

The expression of the recombinant E2 in *N. tabacum*, which is recognized by a specific monoclonal antibody (2.9H), has the ability to generate specific neutralizing antibodies in guinea pigs. These results and those obtained by Aguirreburualde et al. (2013) substantiate more research to establish an alternative plant-based production platform of vaccines against BVDV.

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Chapter 9 Mathematical Modelling in Recombinant Plant Systems: The Challenge to Produce Heterologous Proteins Under GLP/GMP

Abstract In the last time and in the near future, the markets are demanding large recombinant proteins production capacity, due to the production levels of traditional platforms will be certainly not suffice to make available these demands (Huang and McDonald, Biotechnol Adv 30:398–409, 2012). The explore of alternative tools to assure adequate supplies for a growing demand constitutes a challenge of present times being the "bioengineered pharmaceutical plant" a promising strategy to respond to this require at affordable costs. However, as a commercial process requires high productivities and product yield at minimum cost, and, also, regulations must be follows like GMP and GLP. A mathematical model like the ones described in the present chapter allows making predictions and control of biosynthesis and yielding into the process.

Keywords Mathematical modeling • Recombinant proteins-*Nicotiana tabacum-molecular* farming-cell suspension cultures

9.1 Introduction

According to FDA/USDA (2002) "bioengineered pharmaceutical plant" is a plant manipulated by recombinant DNA technology to express a gene encoding a biological or drug product. Plants expressing transiently o constituently recombinant proteins are considered competitive systems for producing high-value recombinant proteins for medical and industrial purposes. This technology (molecular pharming® or biopharming or agropharming) has advanced greatly as a secure technology, capable of rendering valuable recombinant proteins free of toxins and animal pathogens in a relatively short time and cost-effective (Ma et al. 2005; Franconi et al. 2010; De Muynck et al. 2010; Paul and Ma. 2011; Yuan et al. 2011). This scenario opens up promising horizons to produce recombinant proteins with attractive prospects for commercial exploitation. Many proofs of principles studies just to commercialization have been obtained in the last 25 years (Twyman et al. 2003; Arcalis et al. 2013). Sigma-Aldrich commercializes plant-made recombinant avidin and bovine trypsin, Dow AgroSciences LLC produces plant-made recombinant veterinary vaccines and it has recently been approved by FDA the enzyme Taliglucerase alfa, a carrot-expressed recombinant glucocerebrosidase for the treatment of Gaucher disease, to be commercialized by Pfizer (FDA application No (NDA) 022458, 2012). Furthermore, Heber Biotec (Havana, Cuba) has produced the first whole antibody in tobacco plants. It was also demonstrated that most of the recombinant antibodies produced in plants maintains the functional properties as the ones produced in mammalian cell cultures (Kaiser 2008; Zimran et al. 2011; Zeitlin et al. 2011).

9.2 Industrial Production

Manufacturing bioengineered pharmaceutical plants are documented clearly in standard operating procedures (SOPs), Outlines of Production, or other records, following strict regulations (FDA and USDA Regulations 1999, 2002).

Facilities and procedures used for the manufacturing of regulated products, like bioengineered pharmaceutical plants, should be designed following good laboratory practice and good manufacturing processes (GLP and GMP resp.), conditions to ensure pure, sterile, non-toxic, in the case of vaccines assure potency, among other characteristics (Shepherd 1999; EudraLex 2011, ISO 14644-1, Fischer et al. 2012). Product characterization, the manufacturing process, and *in vitro* studies followed by animal studies, are prerequisites to initiating clinical trials. GLP are production and testing practices that helps to ensure a quality product. GLP arranges with the organization, process and conditions under which laboratory studies are planned, performed, monitored, recorded and reported. Also, GLP practices involve a set of regulations designed to establish standards for the conduct and reporting of nonclinical laboratory studies and to ensure the quality and integrity of nonclinical safety data submitted to the regulatory authorities. In that way, GLP data are intended to promote the quality and validity of test data.

GMP has been legislated to pharmaceutical and medical device companies that must follow these procedures, assuring high quality products and batch-to-batch reproducibility. GMPs regulate the manufacture, control, accountability, and documentation of drug or biologic substances and products manufactured for human or veterinary use. The regulations, also, require adequate controls for the release and security of the products before they are allowed to arrive into the general marketplace.

9.3 Industrial Production in Plant Platforms

Plants offer numerous advantages for the production of biopharmaceutical proteins including the capacity to express complex heterologous proteins with posttranslational modifications as glycan patterns and proline hydroxylation among others (Vézina et al. 2009; Eskelin et al. 2009; Gomord et al. 2010; Ahmad et al. 2010;

Xu et al. 2011; Fischer et al. 2012; Strasser 2012). Also, the plant platform has demonstrated to be a secure technology, capable of rendering valuable recombinant proteins free of toxins like retrovirus, prions, mycotoxines and animal pathogens (inherent safety reflecting the inability of human pathogens to replicate in plants) in a relatively short time (Ma et al. 2005; Franconi et al. 2010; De Muynck et al. 2010; Paul and Ma 2011; Yuan et al 2011). Moreover, transient expression has the advantage of a rapid scaled up, therefore offering a rapid response to emerging pandemics or bioterrorism response or the possibility to develop personalized (patient-specific) vaccines (Giritch et al. 2006; Daniell et al. 2009; D'Aoust et al. 2010; Rybicki 2010; Twyman et al. 2012). McCormick et al. (2012) described a plant viral expression system to produce personalized recombinant idiotype vaccines following the concept of a tailor- made programmed. The vaccines against follicular B cell lymphoma were derived from each patient's tumor and it was reported in a phase I clinical trials. Transient tobacco-viral expression system was used for rapid production of the needed amount of idiotype vaccine.

Additionally, other advantages are the low cost of upstream production and the potential for large-scale cultivation (Molina et al. 2004; Escribano and Perez-Filgueira 2009; Thomas et al. 2011; Fischer et al. 2013). The industrial recombinant protein production is achieved by two main platforms: transient expression in plants and fermentation-based platforms with stable expression or transgenic expression in cell suspension cultures.

9.4 Transient Expression Platform

In the last years, bioprocess with binary or viral vectors have also been interested for the rapid and systemic infection and the large amounts of product obtained to achieve an industrial scale. Agro-infiltration, or transient expression system, is a biotechnology method to transiently express a gene during a short period of time without genetic modification (epigenetic modification) in a protoplast, cell, tissue, organ or plant infected. Binary or viral vectors harboring a sequence of the recombinant protein could be introduced in the nucleus of plant target cells by Agrobacterium sp. infection or biobalistic among other technologies (Gleba et al. 2007; Lico et al. 2008; Sainsbury and Lomonossoff 2008; Paul and Ma 2011). The epigenetic expression of the recombinant protein is obtained few days post infection (usually 4-7 days with binary vector or 10-14 days from viral vectors), in significant quantities. After this period of time, the heterologous expression down due to silencing RNAs that encoded to the recombinant protein. Double-stranded RNA is formed between heterologous RNA and complementary endogenous small interfering RNA (siRNA or miRNA). The double strand structure obtained (dsRNA) can trigger posttranscriptional gene silencing (PTGS). The dsRNA activated was cleaved into 22-25 nt RNAs which act as guides to target homologous mRNA sequences for their destruction (Mishra and Mukherjee 2007; Chau and Lee 2007).

For that reason, during transient expression assays never occurred an integration of the transgene into the host genome due to the completely destruction of foreign RNA expression. It is important to point out that transient expression is not considered to be an alteration of genomic plant material and, in consequence, the plant is not considered like GMO (Genetically Modified Organism). Also, cell, tissue, organ or plants transiently transformed do not exhibit macroscopic responses to *A. tume-faciens* infections or bombardment by the gene gun.

The agroinfiltration assays are commonly carried out using *N. tabacum* (tobacco) plants grown in pots and incubated in room chambers. The main reason of use tobacco plants is due to their leaves that are easy to infiltrate and manipulate. Furthermore, tobacco plants are recommended due to the protection against foodchain contamination. Other species agroinfiltrated are tomato and lettuce (Wroblewski et al. 2005).

Also, a variety of strategies were emerging in order to increase yield and achieve an efficient transient platform production during the last decade. One of these emerging technologies is "Magnifection" described as scalable process that can be done on an industrial scale (Gleba et al. 2005). This method involves an efficient vector design carrying T-DNAs encoding RNA replicons combined with and efficient systemic DNA delivery of the viral expression platform by mixing different Agrobacterium lines harbouring fractions of the viral machinery and agrobacteria delivery. In addition, speed, expression level, and yield of a plant RNA virus were drastically increased by altering the codon usage of the virus and the inclusion of typical eukaryotic introns. These modifications were able to the efficiency of delivery, resulting in a reduction in the amount of required infectious agrobacterium (Marillonnet et al. 2005).

In 2006, Bayer and Icon Genetics adopted this methodology and have developed a new production process combining these technologies and transient transformation platform in tobacco plants. Finally, in 2009, Bayer Innovation GmbH present the whole process (http://www.youtube.com/watch?v=fVOBEk5DVZc) following the concept of tailor made pharma.

The FAST technique (Fast Agro-mediated Seedling Transformation) was developed in order to express a wide variety of constructs driven by different promoters in Arabidopsis cotyledons (Li et al. 2009). This method has an especially high potential, ideal for future automated high-throughput analysis (Kolukisaoglu and Thurow 2010). Giritch et al. (2006) using a plant viral vector obtained high expression of heterologous proteins with potential to scale up the process (see below).

ProficiaTM is described as an efficient method to response quickly to emerging diseases (http://www.medicago.com/English/Technologies/Why-Proficia/default.aspx). This platform is described with the high advantage to produce vaccines or therapeutics antibodies in "unmatched speed" obtaining an end product like a vaccine in less than 3 weeks.

Other commercially approaches are extensively reviewed by Paul and Ma (2011).

9.5 Fermentation-Based Platforms

Fermentation-based platforms are carried out in bioreactor batch cell cultures with industrial capacity resulted in high cell densities and production levels. The recombinant or transgenic plants are obtained by introduction a DNA segment (T-DNA), carrying the recombinant protein, into the nucleus of infected plant cells using Agrobacterium tumefaciens as biological delivery system or direct transfer methods like biobalistic, microinjection among others (Alvarez and Marconi 2011). Using either indirect or direct methods, it is possible to introduce foreign DNA into any regenerable plant cell type. Using Agrobacterium technology, the T-DNA plasmid containing the heterologous DNA sequence is hazardous inserted in the plant genome, into a chromosome, by illegitimate recombination or non-homologous end-joining (Somers and Makarevich 2004). The stable transformation using Agrobacterium technologies integrate one copy of T-DNA sequence into the cell genome using a T-vector carrying: the recombinant protein, the selectable and the marker genes. After 48 hs post-infection, the recombinant explants must be isolated from the large excess of untransformed cell population using the selectable marker (like antibiotics, herbicides, among others) allowing the recombinant cells proliferation. Cells that do not have the T-DNA integrated into their genome will die, obtaining uniform (nonchimeric) transformants from vegetatively propagated cells. Cloning transformed cells (calli) are induced from recombinant explants grown in a defined media containing growth regulators.

Transformed cells could be grown as microorganism or animal cell culture, easy to scale up. Plant cell bioreactors are obtained in large scale as a safe, convenient and economical production system for recombination proteins in shorter production cycles. This clean technology, growing transgenic material in a confined environment, has been widely accepted by the public perception due to their biosafety implications.

Geneware® expression technology (www.kbpllc.com) developed by Kentucky BioProcessing, LLC (KBP; Owensboro, KY), is specialized on the expression, extraction, and purification of recombinant proteins from plants at commercial scale level. Sigma-Aldrich Fine Chemicals (SAFC; St. Louis, MI) named in the introduction, produce in plant-based platforms therapeutic protein extraction and purification, bio-conjugates, excipients and adjuvants. Medicago Inc., (Quebec City, Canada) manufacturing capability for plant manipulation, product recovery and purification.

Other companies producing plant-based pharmaceuticals are Protalix (Carmiel, Israel) that utilizes a novel bioreactor for plant cell culture system, ProCellExTM, based on disposable sterile plastic bags; Biolex Therapeutical (Pittsboro, NC) based on the aquatic plant *Lemna minor* (www.biolex.com/lexsystem.htm). PharmaPlanta has a pilot scale facility to produce recombinant subunit vaccines, mAbs and other therapeutic proteins, among other products (Huang and McDonald 2012).

9.6 The Main Problem

Commercialization plant-based expression systems were characterized by the lack of a support for large scale facilities manufacturing these products conform to current Good Laboratory and Manufacturing Practice guidelines. The main obstacles to solve are the lack of reproducibility between batches and the variable expression levels within the batch culture. The variations observed in growth and production is a consequence of plant physiology *per se* with genetic and metabolic regulatory controls characteristic of plant kingdom. In transient expression system, the strict temperature control during the growth of plants at the room chamber and the defined post-infiltration harvest-time and the age of leaves to agroinfiltrate are critical for the reproducibility of the results (Buyel 2013). In batch cultures, the plant cells tend to aggregate, are prone to rapid sedimentation, and are vulnerable to high shear sensitivity. For that reason, the manner in which the bioreactor is operated is critical for the reproducibility of the results (Huang and McDonald 2012; Marconi et al. 2014).

The relationship between relative addition rates of nutrients and relative growth rate varies as an unpredictable function in cells and plants. It is due to plants altering periods of assimilation of nutrients with starving stages. The consequence is a pulse on/off between the high nutrient concentration with high availability and relative growth rate, with starving periods where the growth is arrested (Poorter and Lewis 1986; Cannel and Thornlay 2000). During the assimilation period a relative growth rate could be described as:

$$\boxed{\frac{1}{W}\frac{dW}{dt} = \beta(N - N_{min})}$$

Where W is weight, β is the slope of the response and N is the nitrogen into the plant and N_{min} is the nitrogen at minimal concentration when growth is arrested. The N is integral to the leaf proteins, being of photosynthetic machinery (Wright et al. 2004).

Taking into account these variations, in growth, and as a consequence, in production parameters, mathematical models could be applied to predict the growth of plant cells being useful tools for the industry. Many predictive mathematical models describing the dynamics of biomass growth, product biosynthesis rates and nutrient substrate consumption are derived from microbial cultures. Also, the complexity of models varies enormously, being affected by the abilities, available data and the objectives of the modelers. However, it is expected that a mathematical model can be used to predict or represent or to describe the behavior of a system using mathematical language. Also, models must facilitate process optimization, including of increasing product quality and productivity and reducing manufacturing cost, risk, and time. In the present chapter, two models are present for transient and stably plant and cell cultures.

9.7 Mathematical Modeling for Transient Platform

Johannes F. Buyel (2013) presented an interesting Thesis where a mathematical modeling is developed for plant transient expression systems. The protein model to be express was a monoclonal antibody 2G12 described as specific for the HIV gp120 glycoprotein. Also, a marker protein, DsRED was used as tracer in the experiments. The set of experiments was done using transient expression in *Nicotiana tabacum* var. Petit Havana SR1 by infiltration of leaves with *Agrobacterium tume-faciens* harboring the recombinant plasmid.

The infiltrated leaf was subdivided into four positions parallel to the main vein as a matrix (Fig. 9.1). This variable was indicated by the suffix p. Also, the plant leaves were identified by age since the number 1 assigned for the oldest to the apical leaf (number 8). The suffix to denote the individual leaf into de plant was k (same figure).

The quantity and distribution of the recombinant protein could be processed like a mathematical matrix. The initial concept is described by this equation:

$$C[P] = \frac{m[P]}{V}$$

Where, C[P] is the recombinant protein concentration and m[P] is the mass of the recombinant protein in a known extract volume (V).

The matrix could be described as:

$$\boxed{V_{k,p} = m_{t,k} \cdot \eta_k \cdot \Psi_{k,p} \cdot \epsilon}$$

Where the extract volume (V) for the position p in a k leaf has a mass average of m in this leaf k, η modified by effective biomass ratio for each k leaf (calculated by the intercostal field biomass (g) per biomass extracted (g)) and the position correction Ψ for each leaf k (biomass of position p per biomass extracted in g). Finally, ϵ is the

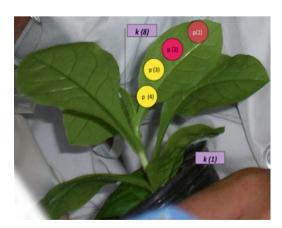


Fig. 9.1 *N. tabacum* leaves to be used to transiently express a protein

extract ratio calculated by the volume of solids-free extract (mL) per biomass extracted (g).

The final recombinant protein yield is obtained from a linear second-order polynomial fit:

$$f(V_{kp}, \beta_k) = \beta_{k,l} + \beta_{k,2} V_{k,p} + \beta_{k,3} (V_{k,p})^2; \beta_k = (\beta_{k,l}, \beta_{k,2}, \beta_{k,3})$$

The study includes a quantitative impact of many parameters, determined and modeled using a design of experimental approach. The post-infiltration incubation temperature, plant and leaf age and incubation time with Agrobacterium were found to be major factors influencing protein yields and growth variation.

9.8 Mathematical Modeling for Fermentation-Based Platforms

The recombinant full antibody r14D9 was used as a protein model to be expressed in *Nicotiana tabacum* cv. Xhanti NN cell suspension cultures (Petruccelli et al. 2006; López et al. 2010). For the bioreactor production, cell suspension expressing the antibody r14D9 with the retention signal KDEL at endoplasmic reticulum were scaled up from a 225 mL Erlenmeyer flask to 2L-bioreactor. Growing cell suspension cultures in a batch bioreactor is often complicated due to the cell aggregation process that leads to the formation of zones where the cell growth is limited. The growth could be restricted by oxygen and nutrients demands, increase the heterogeneity of culture and concentration of toxic substances, among others. Also, plants cells have a critical inoculation density below which growth is arrested. The consequence will be the accumulation of non-dividing cells in a short period of time, and finally aborting the experiments.

Typical slope of the growth kinetics and production of recombinant protein have high standard error with high dispersion of scores around the means (Fig. 9.2). This curves could be characterized with an early exponential period with low recombinant protein production, a gradual slowdown as dividing cell reaches its maximum and a subsequent stationary face (same figure). The recombinant protein production shows more unpredictable features. However, the recombinant protein production curve suggests the production rate follows the dividing or proliferating cells concentration.

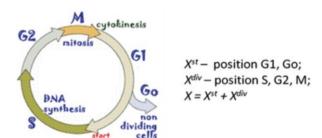


Fig. 9.2 Schematic representation of plant cell cycle

As a result, the cell population rapidly differentiates into dividing (growing and dividing cells) and non-dividing (stable) cells and each population growth with a proper kinetics. Thus, in order to calculate the dynamics of cell growth it is necessary to take into account the difference in energy substrate metabolism of stable and proliferating cells in such zones and use both structured and unstructured models that were previously successfully applied for microbial batch processes (Klykov and Kurakov 2012, 2013).

The mathematical model is based on the theory of energy-limited growth that allows precise evaluation of a cell population age structure into the bioreactor.

The model is based on treating the biomass as two main groups: dividing and non-dividing cells (using a combination of statistical data and qualitative causal assumptions) (Fig. 9.2). Therefore, a phytofermentation process is a "mixture" of cells of different ages being this population characterized by the parameter R:

$$R = \frac{X^{st}}{X}$$

Where Xst is the non-dividing cell concentration at the synchronized degree R, and X is the total biomass. The age structure of the cell population varies, thus characterizing these variations is fundamental for the structured model.

On the other hand, the unstructured model is based on the decrease of the absolute and the specific growth rates of the biomass, as these parameters are directly related to the biomass concentration at the growth limitation phase when oxygen is limited (GIP: growth inhibition phase):

$$A = \frac{m}{a}$$

In this model, the energy substrate consumption rate for viability maintenance (m) is specified by the oxygen and trophic coefficient (a) that is assumed as a constant during GIP. The population is synchronized to non-proliferating cells, which consume oxygen only for primary metabolism.

Equation of the structured model for biomass in the GIP is:

$$\frac{d^{n}X^{div}}{d(X^{st})^{n}} = \frac{K(-1)^{(n-1)}n!}{A^{2}(X^{st})^{(n+1)}} - C$$

Where n - is an integer that specifies the order of the derivative of this function; $X^{div} - is$ the quantity of dividing cells; $X^{st} - is$ the quantity of non-dividing (stable) cells; k - is the overall growth rate multiplied by the rate of accumulation of stable (or non-dividing) cells; A - is the ratio of energy required to maintain viability to energy required for biomass accumulation and/or maintaining the rate of accumulation of stable (non-dividing) cells. In addition, if n = 1 then C = 1, if $n \ge 2$ then C = 0.

The equation of a structured model for substrate (metabolites) in growth inhibition phase is:

$$d(P \text{ or } -S)/d\tau = k^{\text{div}}_{P,S} X^{\text{div}} + k^{\text{st}}_{P,S} X^{\text{st}}$$

P and S symbols are the valuable metabolite and the substrate, respectively, $k^{div}_{P,S}$ and $k^{st}_{P,S}$ coefficients are constants synthesis (utilization) of dividing and non-dividing cells. In this model, it is assumed that metabolites are synthesized only by proliferating (dividing) cells. Non-proliferating (stable) cells, as a rule, destroy these products. Therefore, signs of the constants for metabolite synthesis and degradation are opposite. The same should be stated for substrates utilized for cell construction.

The equation for the unstructured model in growth inhibition phase (GIP) is:

$$\boxed{ X = X_{p} - \left(X_{p} - X_{lim}\right) * exp^{\left(-A*(\tau - \tau lim)\right)} }$$

Where X is the amount of biomass calculated using an unstructured model; X_p – the maximum estimated amount of biomass; X_{Lim} – the amount of biomass at the start of the limitation of cell growth; τ and τ_{lim} are the terms of the estimated time of cultivation and cultivation duration from start until the beginning of the limitation of cell growth.

These equations describe all the known diversity of the processes with S-like growth curves and changes in the concentrations of substances in closed systems, which is an entirely new and previously unknown fact. It is known that a physical law means a generalization of a numerical relationship between the objects of the real physical world that is running under specified conditions for the class of the objects and does not follow from any of the previously discovered laws. There is no reason not to admit the two described equations for the GIP as laws for GIP. The data obtained were used for the selection of techniques to increase the protein expression by genetically modified microorganisms (Klykov et al. 2011).

The proposed modeling approach for the cultivation of plant cells using a structured model reflects the real dynamics of changes in the age structure of cell populations in the batch culture. Isolating growing cells based on physiological age into two groups – dividing and stable cells (non-dividing), allows applying a structured model for scaling up from the bench to a phytofermenter. Processing data, obtained during cultivation and according to the structured model, gives the opportunity to deeper understand the dynamics of changes occurring in the cell population, accurately predict both the dynamics of biomass growth and biosynthesis of a target protein or metabolite and significantly reduce the cost of improving cultivation of cells on an industrial scale.

9.9 Conclusions

Development of transgenic plants is a technology used to basic studies like functional genomics research and, also, in modern plant breeding and in the last years as a platform for recombinant proteins production. There are many protocols to obtain transient or transgenic plants expressing heterologous proteins. In both systems, heterologous protein production like transient platforms or fermentation-based platforms proved to be a suitable process to obtain large- scale productions. However, a commercial process requires high productivities and product yield at minimum cost (Scragg 1992), and, also, regulations must be follows like GMP and GLP. A mathematical model like the ones described before allows making predictions and control of biosynthesis and yielding into the process.

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ERRATUM TO

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This chapter was contributed by three authors. Inadvertently the chapter was published without the below mentioned authors;

P. L. Marconi (🖂)

U. Maimonides-CONICET, Hidalgo 7758, CABA, Argentina e-mail: marconi.patricialaura@maimonides.edu

S. Klykov (\boxtimes)

PHARM-REGION, Ltd, c.1, b.10, Baryshikha street, Moscow, Russia e-mail: SmlK03@mail.ru

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